

SCORE Search Results Details for Application 09556178 and Search Result 20101203_114247_us-09-556-178-1.rag.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101203_114247_us-09-556-178-1.rag.

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GenCore version 6.3
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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:51 ; Search time 74 Seconds
(without alignments)
9429.236 Million cell updates/sec

Title: US-09-556-178-1

Perfect score: 2898

Sequence: 1 MNVVFAVKQYISKMIEDSGP.....GLHRSRSKESSQVTSRSASRR 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6395994 seqs, 1224146475 residues

Total number of hits satisfying chosen parameters: 6395994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_201023:*

1: geneseqpl:*

2: geneseqp2:*

3: geneseqp3:*

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	2898	100.0	570	AAY49958 Human ves
2	2898	100.0	570	Aab03813 Human ves
3	2898	100.0	570	Aab94478 Human pro
4	2898	100.0	570	Ade61224 Human Pro
5	2898	100.0	570	Adp12603 Protein e
6	2898	100.0	570	Adr99181 Vacuolar
7	2898	100.0	570	Ajf47297 Human MCR
8	2898	100.0	570	Aye14424 Allograft
9	2844	98.1	570	Abb57217 Mouse isc
10	2840	98.0	570	Ade61222 Rat Prote
11	2815.5	97.2	578	Abg04478 Novel hum
12	1920	66.3	390	Aao21766 Human rib
13	1584	54.7	574	Abb63752 Drosophil
14	1584	54.7	574	Afb98005 Fruit fly

15	1310	45.2	441	1	ABG04479	Abg04479 Novel hum
16	1299.5	44.8	567	2	AQD50046	Aqd50046 Rice cDNA
17	1286	44.4	568	2	ANL98635	An198635 Oryza sat
18	1270	43.8	567	3	AMV44951	Awy44951 Plant pro
19	1026.5	35.4	210	1	AAY07020	Aay07020 Breast ca
20	976	33.7	577	1	ABR53033	Abr53033 Protein s
21	976	33.7	577	1	ADK62860	Adk62860 Disease t
22	949.5	32.8	472	3	AXH20971	Axh20971 Zea mays
23	786.5	27.1	329	3	AWP61628	Awp61628 Aspergill
24	778.5	26.9	722	1	AAB18291	Aab18291 Plasmodiu
25	753	26.0	364	2	AQD41760	Aqd41760 Rice cDNA
26	714	24.6	165	1	AAO04331	Aao04331 Human pol
27	574	19.8	219	2	ARO38966	Aro38966 Soybean c
28	574	19.8	219	3	AXJ12112	Axj12112 Heteroder
29	510.5	17.6	184	2	ARO77042	Aro77042 Soybean c
30	510.5	17.6	184	3	AXJ50188	Axj50188 Heteroder
31	492	17.0	230	1	AFR53396	Afr53396 Recombina
32	492	17.0	230	3	AXD18698	Axd18698 Sorghum b
33	469.5	16.2	186	2	ARO80389	Aro80389 Soybean c
34	469.5	16.2	186	3	AXJ53535	Axj53535 Heteroder
35	416	14.4	212	3	AWP61629	Awp61629 Aspergill
36	407	14.0	621	2	ARM75723	Arm75723 Arabidops
37	407	14.0	633	1	AAG50809	Aag50809 Arabidops
38	407	14.0	633	2	ALJ97173	Alj97173 Plant pro
39	407	14.0	653	2	ARM75722	Arm75722 Arabidops
40	407	14.0	662	1	AAG50808	Aag50808 Arabidops
41	407	14.0	662	2	ALJ97172	Alj97172 Plant pro
42	401	13.8	633	1	AAG18696	Aag18696 Arabidops
43	401	13.8	633	2	ALJ52955	Alj52955 Plant pro
44	401	13.8	633	2	ARM38817	Arm38817 Arabidops
45	401	13.8	662	1	AAG18695	Aag18695 Arabidops

ALIGNMENTS

RESULT 1
 AAY49958
 ID AAY49958 standard; protein; 570 AA.
 XX
 AC AAY49958;
 XX
 DT 15-JUN-2007 (revised)
 DT 04-FEB-2000 (first entry)
 XX
 DE Human vesicle trafficking protein 1.
 XX
 KW Human; vesicle trafficking protein; VTP-1; VTP-2; VTP-3; apoptosis;
 KW cancer; inflammation; BOND_PC; vacuolar protein sorting 45A;
 KW leucocyte vacuolar protein sorting 45;
 KW vacuolar protein sorting 45B (yeast);
 KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;
 KW VPS45B; VPS54A; VSP45A; HVPS45;
 KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;
 KW vacuolar protein sorting 45A (yeast), isoform CRA_a;
 KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];
 KW vacuolar protein sorting 45A (yeast);
 KW vacuolar protein sorting 45A (yeast) [Homo sapiens];
 KW vacuolar protein sorting 45 homolog (S. cerevisiae);
 KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];
 KW vacuolar protein sorting 45 isoform;
 KW vacuolar protein sorting 45 isoform [Homo sapiens];
 KW unnamed protein product; unnamed protein product [Homo sapiens]; G05764;
 KW G05798; G06886; G06904; G06954; G016020; G016192.
 XX
 OS Homo sapiens.
 XX

PN US5989859-A.
 XX
 PD 23-NOV-1999.
 XX
 PF 07-NOV-1997; 97US-00967364.
 XX
 PR 07-NOV-1997; 97US-00967364.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Bandman O, Guegler KJ, Corley NC, Lal P, Shah P;
 XX
 DR WPI; 2000-022782/02.
 DR N-PSDB; AAZ35833.
 DR PC:NCBI; gi18105063.
 DR PC:SWISSPROT; Q9NRW7.
 DR PC:BIND; 261868, 261869.
 XX
 PT Novel vesicle trafficking proteins used in the diagnosis, prevention, and treatment of inflammation or cancer.
 XX
 PS Claim 9; Fig 1; 55pp; English.
 XX
 CC The present sequence represents the human vesicle trafficking protein designated VTP-1. VTPs can be used in a method for preventing or treating disease associated with an increase in apoptosis. The method can treat diseases such as cancer and inflammation, by administering a VTP antagonist
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed information from BOND.
 XX
 SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||
 Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||
 Qy 61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYIFIYSNVISKSVDVKSLSAEADEQEVVVA 120
 |||||||
 Db 61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYIFIYSNVISKSVDVKSLSAEADEQEVVVA 120
 |||||||
 Qy 121 EVQEFGYGDYIAVNPHFLSFLNILGCCQGRNWDPQLSRTTQGLTALLSSLKKCPMIRYQLS 180
 |||||||
 Db 121 EVQEFGYGDYIAVNPHFLSFLNILGCCQGRNWDPQLSRTTQGLTALLSSLKKCPMIRYQLS 180
 |||||||
 Qy 181 SEAARKLAECKVKQVITKEYELFEPFRTEVPPLLLIDLRCCDAITPPLNQWTYQAMVHELL 240
 |||||||
 Db 181 SEAARKLAECKVKQVITKEYELFEPFRTEVPPLLLIDLRCCDAITPPLNQWTYQAMVHELL 240
 |||||||
 Qy 241 GINNNRIDSLSRVPGISKDLREVVVLSAENDEFYANNMYLNAEIGSNIKNLMEDFQKKPK 300
 |||||||
 Db 241 GINNNRIDSLSRVPGISKDLREVVVLSEADNFYANNMYLNAEIGSNIKNLMEDFQKKPK 300
 |||||||
 Qy 301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
 |||||||
 Db 301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
 |||||||
 Qy 361 NDHSSALQNIKRLLNQPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEKRY 420
 |||||||
 Db 361 NDHSSALQNIKRLLNQPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEKRY 420
 |||||||
 Qy 421 KLVSADVVEYGGKRVRGSDLFSPKDAVITKQFLKGLKGVENVYQTQHQPLHETLDHLIKG 480

Db	421	KLVSAAVEYGGKVRGSDLFSPKDAVATKQFLKGKGVENVYTQHQPFHLHETLDHLIKG	480	
Oy	481	RLKENLYPYLGPSTLRDRPQDIIIVFVIGGATYEEALT	VYLNRLTPGVRIVLGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIIVFVIGGATYEEALT	VYLNRLTPGVRIVLGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRASRR	570	
Db	541	KSFLEEVLASGLHSRSKESSQVTSRASRR	570	

RESULT 2

AAB03813

ID AAB03813 standard; protein; 570 AA.

XX

AC AAB03813;

XX

DT 15-JUN-2007 (revised)

DT 13-OCT-2000 (first entry)

XX

DE Human vesicle trafficking protein-1 (VTP-1) amino acid sequence.

XX

KW Vesicle trafficking protein; VTP-1; human; cancer; inflammation; asthma;
 KW foetal development; Crohn's disease; diabetes; multiple sclerosis;
 KW rheumatoid arthritis; infection; ulcerative colitis; proliferation;
 KW irritable bowel syndrome; apoptosis; AIDS; Alzheimer's disease;
 KW Parkinson's disease; osteoporosis; wasting disorder; BOND_PC;
 KW vacuolar protein sorting 45B (yeast); leucocyte vacuolar protein sorting 45;
 KW vacuolar protein sorting 45B (yeast);
 KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;
 KW VPS45B; VPS45A; VSP45A; HIVPS45;
 KW vacuolar protein sorting 45A (yeast homolog); VPS45A, VPS45B;
 KW vacuolar protein sorting 45A (yeast), isoform CRA_a;
 KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];
 KW vacuolar protein sorting 45A (yeast);
 KW vacuolar protein sorting 45A (yeast) [Homo sapiens];
 KW vacuolar protein sorting 45 homolog (S. cerevisiae);
 KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];
 KW vacuolar protein sorting 45 isoform;
 KW vacuolar protein sorting 45 isoform [Homo sapiens];
 KW unnamed protein product; unnamed protein product [Homo sapiens]; GO5764;
 KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.

XX

OS Homo sapiens.

XX

PN US6071703-A.

XX

PD 06-JUN-2000.

XX

PF 04-AUG-1999; 99US-00368408.

XX

PR 07-NOV-1997; 97US-00967364.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Guegler KJ, Shah P, Corley NC, Bandman O, Lal P;

XX

DR WPI; 2000-422079/36.

DR N-PSDB; AAA59873.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX

PT Identifying polynucleotides encoding vesicle trafficking proteins (VTP)

PT for treating and preventing e.g. inflammation, by detecting a

PT hybridization complex of a nucleic acid from a sample and a

PT polynucleotide encoding a VTP.

XX

PS Example; Fig 1; 55pp; English.

XX

CC This sequence represents human vesicle trafficking protein (VTP-1) amino acid sequence. VTP-1 encoding cDNA was isolated from a THP-1 cell line CC cDNA library (THP1PEB01). VTP-1 has structural and chemical homology with CC a mouse vacuolar protein-sorting protein mVps45. The present invention CC relates to a method for detecting human VTP encoding polynucleotide CC sequences and includes nucleotide and protein sequences for human VTP-1, CC VTP-2 and VTP-3. Northern analysis of VTP-1, 2, and 3 shows that their CC expression is associated with cancer, inflammation and foetal/infant CC development. The method of the invention is useful for screening and CC identifying a polynucleotide encoding a human VTP, which may be used for CC the diagnosis, prevention, or treatment of inflammation associated CC disorder, e.g. asthma, Crohn's disease, diabetes, multiple sclerosis, CC rheumatoid arthritis, infections, ulcerative colitis and irritable bowel CC syndrome. Other diseases and disorders identified, prevented or treated CC with polynucleotide sequences encoding VTP include those associated with CC cell proliferation or apoptosis, such as AIDS, Alzheimer's disease, CC Parkinson's disease, osteoporosis, wasting diseases and cancer

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX

SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60

|||||||

Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60

|||||||

Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRKPKYTIYIFIYFSNVISKSDVKS LAEADEQEVV A 120

|||||||

Db 61 EIMKHLKAICFLRPTKENVDYIIQELRKPKYTIYIFIYFSNVISKSDVKS LAEADEQEVV A 120

|||||||

Qy 121 EVQEFGYGDYIAVNPHLSFLNILGCCGQRNNWDPQLSRTTQGLTALLLSSLKKCPMIRYQL S 180

|||||||

Db 121 EVQEFGYGDYIAVNPHLSFLNILGCCGQRNNWDPQLSRTTQGLTALLLSSLKKCPMIRYQL S 180

|||||||

Qy 181 SEAARKLAECVKQVITKEYELFEFRRTEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL 240

|||||||

Db 181 SEAARKLAECVKQVITKEYELFEFRRTEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL 240

|||||||

Qy 241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNAEIGSNIKNL MEDFQKKPK 300

|||||||

Db 241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNAEIGSNIKNL MEDFQKKPK 300

|||||||

Qy 301 EQQKLESIADMKA FVENYPQFKKMSGTVKHVTVGELSRLVSE RNLLLEVSEVEQELAC Q 360

|||||||

Db 301 EQQKLESIADMKA FVENYPQFKKMSGTVKHVTVGELSRLVSE RNLLLEVSEVEQELAC Q 360

|||||||

Qy 361 NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKG VSEK YR 420

|||||||

Db 361 NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKG VSEK YR 420

|||||||

Qy 421 KLVS AVEYGGKVRGSDLFSPKDAV AITKQFLKG LKG VENV YTQHPFLHETLDH LIKG 480

|||||||

Db 421 KLVS AVEYGGKVRGSDLFSPKDAV AITKQFLKG LKG VENV YTQHPFLHETLDH LIKG 480

|||||||

Qy 481 RLKENLYPYLGPSTL RDRPQD II V FVIGGAT YEE ALTVY NLNRTTPGV RIVLG GTTV HNT 540

|||||||

Db 481 RLKENLYPYLGPSTL RDRPQD II V FVIGGAT YEE ALTVY NLNRTTPGV RIVLG GTTV HNT 540

|||||||

Qy 541 KSFLEEVLASGLHRSRKESSQVTSRSASRR 570
 ||||||| ||||| ||||| ||||| ||||| |||||
 Db 541 KSFLEEVLASGLHRSRKESSQVTSRSASRR 570

RESULT 3

AAB94478

ID AAB94478 standard; protein; 570 AA.

XX

AC AAB94478;

XX

DT 15-JUN-2007 (revised)

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:15151.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy;

KW BOND_PC; vacuolar protein sorting 45A;

KW leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS45A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS45A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; G05764;

KW G05798; G06886; G06904; G06954; G016020; G016192.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC FOR BIOTECHNOLOGY.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX

PS Claim 8; SEQ ID NO 15151; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-

CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 present invention

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||

Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRKPKYTIYIFIYFSNVISKSDVKS LAEADEQE VVA 120
 |||||||

Db 61 EIMKHLKAICFLRPTKENVDYIIQELRKPKYTIYIFIYFSNVISKSDVKS LAEADEQE VVA 120

Qy 121 EVQEFGYGDYIAVNPHLSFLNILGCCGGRNNWDPQLSRTTQGLTALLLSLKCPMIRYQLS 180
 |||||||

Db 121 EVQEFGYGDYIAVNPHLSFLNILGCCGGRNNWDPQLSRTTQGLTALLLSLKCPMIRYQLS 180

Qy 181 SEAARKLAECVKQVITKEYELFEFRRTEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL 240
 |||||||

Db 181 SEAARKLAECVKQVITKEYELFEFRRTEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL 240

Qy 241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNAEIGSNIKNL MEDFQKKPK 300
 |||||||

Db 241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNAEIGSNIKNL MEDFQKKPK 300

Qy 301 EQQKLESIADMKA FVENYPQFKKMSGTVKHTVVGELSRLVSE RNLLLEVSEVEQELACQ 360
 |||||||

Db 301 EQQKLESIADMKA FVENYPQFKKMSGTVKHTVVGELSRLVSE RNLLLEVSEVEQELACQ 360

Qy 361 NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKG VSEK YR 420
 |||||||

Db 361 NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKG VSEK YR 420

Qy 421 KLVS AAVVEYGGKVRGSDLFSPKDAV AITKQFLKGLKG VENV YTQHQPFLHETLDH LIKG 480
 |||||||

Db 421 KLVS AAVVEYGGKVRGSDLFSPKDAV AITKQFLKGLKG VENV YTQHQPFLHETLDH LIKG 480

Qy 481 RLKENLYPYLGPSTL RDRP QD IIIVFVIGGATYEEALT VYLN R TTPGV RIVLG GTTV HNT 540
 |||||||

Db 481 RLKENLYPYLGPSTL RDRP QD IIIVFVIGGATYEEALT VYLN R TTPGV RIVLG GTTV HNT 540

Qy 541 KSFLEEVLASGLHRSRKESSQVTSRSASRR 570
 |||||||||||||||||||||||||||||||
 Db 541 KSFLEEVLASGLHRSRKESSQVTSRSASRR 570

RESULT 4

ADE61224

ID ADE61224 standard; protein; 570 AA.

XX

AC ADE61224;

XX

DT 15-JUN-2007 (revised)

DT 29-JAN-2004 (first entry)

XX

DE Human Protein NP_009189, SEQ ID NO 7142.

XX

KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung; BOND_PC; vacuolar protein sorting 45A;
 KW leucocytic vacuolar protein sorting 45;
 KW vacuolar protein sorting 45B (yeast);
 KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;
 KW VPS45B; VPS45A; VSP45A; H1VPS45;
 KW vacuolar protein sorting 45A (yeast homolog); VPS45A, VPS45B;
 KW vacuolar protein sorting 45A (yeast), isoform CRA_a;
 KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];
 KW vacuolar protein sorting 45A (yeast);
 KW vacuolar protein sorting 45A (yeast) [Homo sapiens];
 KW vacuolar protein sorting 45 homolog (S. cerevisiae);
 KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];
 KW vacuolar protein sorting 45 isoform;
 KW vacuolar protein sorting 45 isoform [Homo sapiens];
 KW unnamed protein product; unnamed protein product [Homo sapiens]; GO5764;
 KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; NP_009189.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC: BIND; 261868, 261869.

XX

PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
Qy	61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYFIYFSNVISKSDVKS LAEAD EQEVVA 120
Db	61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYFIYFSNVISKSDVKS LAEAD EQEVVA 120
Qy	121 EVQEFGDYIAVNPHLFLSNILGCCQGRNWDPQAQLSRTTQGLTALLSLKKCPMIRYQLS 180
Db	121 EVQEFGDYIAVNPHLFLSNILGCCQGRNWDPQAQLSRTTQGLTALLSLKKCPMIRYQLS 180
Qy	181 SEAARKLAECAVKQVITKEYELFEFRTEVPPLLLILDRCDDA1TPLLNNQWTYQAMVHELL 240
Db	181 SEAARKLAECAVKQVITKEYELFEFRTEVPPLLLILDRCDDA1TPLLNNQWTYQAMVHELL 240
Qy	241 GINNNRIDLSRVPGISKDLREVVL SAENDEFYANNMYLNFAEIGSNIKNL MEDFQKKPK 300
Db	241 GINNNRIDLSRVPGISKDLREVVL SAENDEFYANNMYLNFAEIGSNIKNL MEDFQKKPK 300
Qy	301 EQQKLESIADMKA FVENYQPQFKMSGTVSKHVTVVGELSRLVSE RNLLLEVSE VEQELACQ 360
Db	301 EQQKLESIADMKA FVENYQPQFKMSGTVSKHVTVVGELSRLVSE RNLLLEVSE VEQELACQ 360
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMM DLRNKGVSEK YR 420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMM DLRNKGVSEK YR 420
Qy	421 KLVSAVVEYGGKRVRGSDLFSPKD AVAITKQFLKGLKG VENV YTQHQPF LHE TLDH LIKG 480
Db	421 KLVSAVVEYGGKRVRGSDLFSPKD AVAITKQFLKGLKG VENV YTQHQPF LHE TLDH LIKG 480
Qy	481 RLKENLYP LGPSTL RDRP QDI I FVPIGGAT YEE ALTV NLN RTTPGVRIVL GGTT VHNT 540

Db 481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGTTVHNT 540
 Qy 541 KSFLEEVLASGLHSRSKESQSQTTSRSASRR 570
 |||||||
 Db 541 KSFLEEVLASGLHSRSKESQSQTTSRSASRR 570

RESULT 5
 ADP12603
 ID ADP12603 standard; protein; 570 AA.
 XX
 AC ADP12603;
 XX
 DT 15-JUN-2007 (revised)
 DT 12-AUG-2004 (first entry)
 XX
 DE Protein encoded by mRNA of the invention #213.
 XX
 KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; BOND_PC;
 KW vacuolar protein sorting 45A; leucocyte vacuolar protein sorting 45;
 KW vacuolar protein sorting 45B (yeast);
 KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;
 KW VPS45B; VPS54A; VSP45A; H1VPS45;
 KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;
 KW vacuolar protein sorting 45A (yeast), isoform CRA_a;
 KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];
 KW vacuolar protein sorting 45A (yeast);
 KW vacuolar protein sorting 45A (yeast) [Homo sapiens];
 KW vacuolar protein sorting 45 homolog (S. cerevisiae);
 KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];
 KW vacuolar protein sorting 45 isoform;
 KW vacuolar protein sorting 45 isoform [Homo sapiens];
 KW unnamed protein product; unnamed protein product [Homo sapiens]; G05764;
 KW G05798; G06886; G06904; G06954; G016020; G016192.
 XX
 OS Homo sapiens.
 XX
 PN WO2004042346-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-00131831.
 PR 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX
 DR WPI; 2004-400724/37.
 DR PC:NCBI; gi18105063.
 DR PC:SWISSPROT; Q9NRW7.
 DR PC:BIND; 261868, 261869.
 XX
 PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 65; SEQ ID NO 2612; 1762pp; English.
 XX
 CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The

CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC protein that is encoded by the mRNA of the invention.
 CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||

Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy 61 EIMKHLKAICFLRPTKENVDYI IQELRRPKTYI FIFIYFSNVISKSDVKS LAEADEQEVVA 120
 |||||||

Db 61 EIMKHLKAICFLRPTKENVDYI IQELRRPKTYI FIFIYFSNVISKSDVKS LAEADEQEVVA 120

Qy 121 EVQE FYG DYIAVN PHL FS LN ILGCC QGR NW DPA QLS RTT QGL T ALL LSL KCP MIR YQLS 180
 |||||||

Db 121 EVQE FYG DYIAVN PHL FS LN ILGCC QGR NW DPA QLS RTT QGL T ALL LSL KCP MIR YQLS 180

Qy 181 SEA AKRLAECV KVQ VITKEY L E FFR T E V P P L L I L D R C D D A I T P L N Q W T Y Q A M V H E L L 240
 |||||||

Db 181 SEA AKRLAECV KVQ VITKEY L E FFR T E V P P L L I L D R C D D A I T P L N Q W T Y Q A M V H E L L 240

Qy 241 GIN NN R ID L S R V P G I S K D L R E V V L S A E N D E F Y A N N M Y L N F A E I G S N I K N L M E D F Q K K P K 300
 |||||||

Db 241 GIN NN R ID L S R V P G I S K D L R E V V L S A E N D E F Y A N N M Y L N F A E I G S N I K N L M E D F Q K K P K 300

Qy 301 EQ Q K L E S I A D M K A F V E N Y P Q F K K M S G T V S K H T V V G E L S R L V S E R N L L E V S E V E Q E L A C Q 360
 |||||||

Db 301 EQ Q K L E S I A D M K A F V E N Y P Q F K K M S G T V S K H T V V G E L S R L V S E R N L L E V S E V E Q E L A C Q 360

Qy 361 NDH S S A L Q N I K R L L Q N Q P K V T E F D A A R L V M L Y A L H Y E R H S S N S L P G L M M D L R N K G V S E K Y R 420
 |||||||

Db 361 NDH S S A L Q N I K R L L Q N Q P K V T E F D A A R L V M L Y A L H Y E R H S S N S L P G L M M D L R N K G V S E K Y R 420

Qy 421 K L V S A V V E Y G G K R V R G S D L F S P K D A V A I T K Q F L K G L K G V E N V Y T Q H Q P F L H E T L D H L I K G 480
 |||||||

Db 421 K L V S A V V E Y G G K R V R G S D L F S P K D A V A I T K Q F L K G L K G V E N V Y T Q H Q P F L H E T L D H L I K G 480

Qy 481 R L K E N L Y P Y L G P S T L R D R P Q D I I V F V I G G A T Y E E A L T V Y V N L N R T T P G V R I V L G G T T V H N T 540
 |||||||

Db 481 R L K E N L Y P Y L G P S T L R D R P Q D I I V F V I G G A T Y E E A L T V Y V N L N R T T P G V R I V L G G T T V H N T 540

Qy 541 K S F L E V L A S G L H S R S K E S S Q V T S R S A S R R 570
 |||||||

Db 541 K S F L E V L A S G L H S R S K E S S Q V T S R S A S R R 570

RESULT 6

ADR99181

ID ADR99181 standard; protein; 570 AA.

XX

AC ADR99181;

XX

DT 15-JUN-2007 (revised)
 DT 02-DEC-2004 (first entry)
 XX
 DE Vacuolar protein sorting 45A, VSP45A, SEQ ID 187.
 XX
 KW Cytostatic; breast cancer; cancer; human; Vacuolar protein sorting 45A;
 KW VSP45A; BOND_PC; vacuolar protein sorting 45A;
 KW leucocyte vacuolar protein sorting 45;
 KW vacuolar protein sorting 45B (yeast);
 KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;
 KW VPS45B; VPS54A; VSP45A; H1VPS45;
 KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;
 KW vacuolar protein sorting 45A (yeast), isoform CRA_a;
 KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];
 KW vacuolar protein sorting 45A (yeast);
 KW vacuolar protein sorting 45A (yeast) [Homo sapiens];
 KW vacuolar protein sorting 45 homolog (S. cerevisiae);
 KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];
 KW vacuolar protein sorting 45 isoform;
 KW vacuolar protein sorting 45 isoform [Homo sapiens];
 KW unnamed protein product; unnamed protein product [Homo sapiens]; G05764;
 KW G05798; G06886; G06904; G06954; G016020; G016192.
 XX
 OS Homo sapiens.
 XX
 PN WO2004078035-A2.
 XX
 PD 16-SEP-2004.
 XX
 PF 27-FEB-2004; 2004WO-US007268.
 XX
 PR 28-FEB-2003; 2003US-0450655P.
 XX
 PA (FARB) BAYER PHARM CORP.
 XX
 PI Eveleigh D, Bigwood D;
 XX
 DR WPI; 2004-653556/63.
 DR N-FSDB; ADR99054.
 DR PC:NCBI; gi18105063.
 DR PC:SWISSPROT; Q9NRW7.
 DR PC:BIND; 261868, 261869.
 XX
 PT Diagnosing breast cancer comprises comparing the level of expression of genes or gene products in a first biological sample taken from a patient with that in a normal patient sample.
 XX
 PS Claim 3; SEQ ID NO 187; 53pp; English.
 XX
 CC The present invention relates to a method (M1) for diagnosing breast cancer in a patient. The method comprises comparing the level of expression of one or more genes or gene products in a biological sample from the patient with that in a normal patient sample, where a difference in the gene expression in the first sample compared to that in the second sample is a diagnostic of the disease. Also claimed are: method (M2) for distinguishing between normal and disease tissues; method (M3) for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent; method (M4) for identifying a compound for treating breast cancer; and an array for distinguishing between normal and disease tissues comprising two or more probes corresponding to genes selected from ADR98995-ADR99121 or comprising two or more polypeptides selected from ADR99122-ADR99248. In M1 and M2 the genes are selected from ADR98995-ADR99121 and the gene products are polypeptides selected from ADR99122-ADR99248. M1 is useful for diagnosing breast cancer. M2 and the array are useful for distinguishing between normal and disease tissue. M3 is useful for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent. M4 is useful for identifying a compound for

CC treating breast cancer. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](ftp://ftp.wipo.int/pub/published_pct_sequences).
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVPAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||
 Db 1 MNVVPAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||
 Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIIFYFSNVISKSDVKS LAEADEQE VVA 120
 |||||||
 Db 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIIFYFSNVISKSDVKS LAEADEQE VVA 120
 |||||||
 Qy 121 EVQEFGYGDYIAVNPHLFLSNILGCCQGRNWDPQAQLSRTTQGLTALLSLKKCPMIRYQLS 180
 |||||||
 Db 121 EVQEFGYGDYIAVNPHLFLSNILGCCQGRNWDPQAQLSRTTQGLTALLSLKKCPMIRYQLS 180
 |||||||
 Qy 181 SEA A KRLAECVKQVITKEYLEF RTRTEVPPLLL LIDRCDDA ITPLLNQWTYQAMVHELL 240
 |||||||
 Db 181 SEA A KRLAECVKQVITKEYLEF RTRTEVPPLLL LIDRCDDA ITPLLNQWTYQAMVHELL 240
 |||||||
 Qy 241 GINNNRIDLSRVPGISKD LREVV VLSAENDEF YAN NM YLNF AEIGSNIKNL MEDFQKKPK 300
 |||||||
 Db 241 GINNNRIDLSRVPGISKD LREVV VLSAENDEF YAN NM YLNF AEIGSNIKNL MEDFQKKPK 300
 |||||||
 Qy 301 EQQKLES IADMKAFV ENY P QFKKMS GTVSKHVT VVGELS RL VSERN LLEV SVE QELACQ 360
 |||||||
 Db 301 EQQKLES IADMKAFV ENY P QFKKMS GTVSKHVT VVGELS RL VSERN LLEV SVE QELACQ 360
 |||||||
 Qy 361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKG VSE KYR 420
 |||||||
 Db 361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKG VSE KYR 420
 |||||||
 Qy 421 KLVS AVVEYGGKRVRGSDL FSPKDAV AITKQFLKGLKG VEN VYTQHQPF LHETLDHLIK G 480
 |||||||
 Db 421 KLVS AVVEYGGKRVRGSDL FSPKDAV AITKQFLKGLKG VEN VYTQHQPF LHETLDHLIK G 480
 |||||||
 Qy 481 RLKENLYP YLGPSTL RD RPQD II VFI GGAT YEE ALTVY NLN RTTPG VRIV LG GTT VHNT 540
 |||||||
 Db 481 RLKENLYP YLGPSTL RD RPQD II VFI GGAT YEE ALTVY NLN RTTPG VRIV LG GTT VHNT 540
 |||||||
 Qy 541 KSFLEEV L ASGLH SRS KESS QV TSRSAS RR 570
 |||||||
 Db 541 KSFLEEV L ASGLH SRS KESS QV TSRSAS RR 570

RESULT 7
 AJF47297
 ID AJF47297 standard; protein; 570 AA.

XX
 AC AJF47297;
 XX
 DT 01-NOV-2007 (first entry)
 XX
 DE Human MCR vacuolar protein sorting 45A (VPS45A).
 XX
 KW Diagnosis; prognosis; prophylaxis; therapeutic; drug screening;
 KW diagnostic; transgenic animal; pharmacogenetics; cancer;
 KW multiple myeloma; cytostatic; melanoma; breast tumor; lung tumor;

KW colorectal tumor; prostate tumor; pancreas tumor; stomach tumor;
 KW ovary tumor; bladder tumor; brain tumor; central nervous system tumor;
 KW esophagus tumor; uterine cervix tumor; uterus tumor;
 KW endometrioid carcinoma; mouth tumor; pharynx tumor; liver tumor;
 KW renal tumor; testis tumor; biliary tumor; thyroid tumor; adrenal tumor;
 KW osteosarcoma; chondrosarcoma; hematological tumor; macroglobulinemia;
 KW gammopathy; amyloidosis; tumor marker; BOND_PC;
 KW vacuolar protein sorting 45A; leucocyte vacuolar protein sorting 45;
 KW vacuolar protein sorting 45B (yeast); VPS45A; H1; VPS45; VSP45; VPS45B;
 KW VPS54A; VSP45A; H1VPS45; vacuolar protein sorting 45A (yeast homolog);
 KW VPS54A; VPS45B; vacuolar protein sorting 45A (yeast), isoform CRA_a;
 KW vacuolar protein sorting 45A (yeast);
 KW vacuolar protein sorting 45 homolog (*S. cerevisiae*);
 KW vacuolar protein sorting 45 isoform; unnamed protein product; GO5764;
 KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.
 XX
 OS Homo sapiens.
 XX
 PN WO2007095186-A2.
 XX
 PD 23-AUG-2007.
 XX
 PF 13-FEB-2007; 2007WO-US003697.
 XX
 PR 14-FEB-2006; 2006US-0773072P.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Depinho RA;
 XX
 DR WPI; 2007-701669/65.
 DR N-PDB; AJF46910.
 DR REFSEQ; NP_009190.
 DR PC:NCBI; gi18105063.
 DR PC:SWISSPROT; Q9NRW7.
 DR PC:BIND; 261868, 261869.
 XX
 PT Assessing whether a subject is afflicted with cancer for treating or
 PT preventing cancer comprises determining an altered copy number of a
 PT minimal common region (MCR) in a subject sample compared to a normal copy
 PT number of the MCR.
 XX
 PS Disclosure; Page; 158pp; English.
 XX
 CC The present invention provides a method for assessing whether a subject
 CC is afflicted with cancer or at risk for developing cancer. The method
 CC involves comparing the copy number of a minimal common region (MCR) in a
 CC subject sample to the normal copy number of the MCR, where an altered
 CC copy number of the MCR in the sample and/or alterations in the amount,
 CC structure and/or activity of one or more of the markers (PRKCi5, SEMA4A,
 CC DHH36, GPR86 and combinations thereof) indicates that the subject is
 CC afflicted with cancer or at risk for developing cancer. The invention is
 CC useful for the diagnosis, prognosis, prevention and treatment of cancers
 CC such as B cell cancer, multiple melanoma, myleoma, breast cancer, lung
 CC cancer, bronchus cancer, colorectal cancer, prostate cancer, pancreatic
 CC cancer, stomach cancer, ovarian cancer, urinary bladder cancer, brain or
 CC central nervous system cancer, peripheral nervous system cancer,
 CC esophageal cancer, cervical cancer, uterine or endometrial cancer, cancer
 CC of the oral cavity or pharynx, liver cancer, kidney cancer, testicular
 CC cancer, biliary tract cancer, small bowel or appendix cancer, salivary
 CC gland cancer, thyroid gland cancer, adrenal gland cancer, osteosarcoma,
 CC chondrosarcoma and cancer of hematological tissues and also Waldenstrom's
 CC macroglobulinemia, heavy chain diseases (alpha chain disease, gamma chain
 CC disease, mu chain disease, benign monoclonal gammopathy and immunocytic
 CC amyloidosis. The invention is also useful in diagnostic assays,
 CC pharmacogenomics, drug screening and in the production of transgenic
 CC animals. The present sequence is a human minimal common region (MCR)

CC protein. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at [ftp.wipo.int/pub/published_pct_sequences](ftp://ftp.wipo.int/pub/published_pct_sequences).
 CC
 Revised record issued on 18-OCT-2007 : Enhanced with precomputed
 information from BOND.
 XX
 SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 2; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVPAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||
 Db 1 MNVVPAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||
 Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIIFYFSNVISKSDVKS LAEADEQE VVA 120
 |||||||
 Db 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIIFYFSNVISKSDVKS LAEADEQE VVA 120
 |||||||
 Qy 121 EVQE FYG DYIAVNPHLFLS NILGCCQGR NWDP AQL SRTT QGL TALLSL KCP MIR YQL S 180
 |||||||
 Db 121 EVQE FYG DYIAVNPHLFLS NILGCCQGR NWDP AQL SRTT QGL TALLSL KCP MIR YQL S 180
 |||||||
 Qy 181 SEA AKRLAECV KQV ITKEY LFE FRR TEV PPLL LIDRC DDA ITPL LNQ WTY QAM VHELL 240
 |||||||
 Db 181 SEA AKRLAECV KQV ITKEY LFE FRR TEV PPLL LIDRC DDA ITPL LNQ WTY QAM VHELL 240
 |||||||
 Qy 241 GINNNR IDLS RVP GISK DKL REV VLS AEN DEF YAN NM YLN FA EIG SN IKNL MED FQ KKP K 300
 |||||||
 Db 241 GINNNR IDLS RVP GISK DKL REV VLS AEN DEF YAN NM YLN FA EIG SN IKNL MED FQ KKP K 300
 |||||||
 Qy 301 EQ QK LES IAD MKAF VEN YPQ FK KM SGTV SKH VT V GEL SR LV SER NL LEV SVE VE QEL ACQ 360
 |||||||
 Db 301 EQ QK LES IAD MKAF VEN YPQ FK KM SGTV SKH VT V GEL SR LV SER NL LEV SVE VE QEL ACQ 360
 |||||||
 Qy 361 NDHSS ALQNI KRL LQNP KVTE F DAAR LVML YAL HYER HSSN SL PG LMM DL R NK GV SE KYR 420
 |||||||
 Db 361 NDHSS ALQNI KRL LQNP KVTE F DAAR LVML YAL HYER HSSN SL PG LMM DL R NK GV SE KYR 420
 |||||||
 Qy 421 KL VSAV VEY GGK RV RG SD LF SPK DAVA IT KQF LKG LKG VEN VY TQH QPFL HET LDH LI KG 480
 |||||||
 Db 421 KL VSAV VEY GGK RV RG SD LF SPK DAVA IT KQF LKG LKG VEN VY TQH QPFL HET LDH LI KG 480
 |||||||
 Qy 481 RL KEN LY PYL GP STL RD RP QD II IVF VIGG AT YEE AL T VY NL NR TT PG VR IV LG GT TV HNT 540
 |||||||
 Db 481 RL KEN LY PYL GP STL RD RP QD II IVF VIGG AT YEE AL T VY NL NR TT PG VR IV LG GT TV HNT 540
 |||||||
 Qy 541 KS FLE EV L AS GL HSR SK ESS QV TS RS A S RR 570
 |||||||
 Db 541 KS FLE EV L AS GL HSR SK ESS QV TS RS A S RR 570

RESULT 8
 AYE14424
 ID AYE14424 standard; protein; 570 AA.
 XX
 AC AYE14424;
 XX
 DT 02-SEP-2010 (first entry)
 XX
 DE Allograft rejection diagnosis/prognosis marker protein, SEQ:2612.
 XX
 KW diagnostic test; gene expression; heart transplant rejection;
 KW immunosuppressive; prognosis; rna quantitation; transplant rejection;
 KW BOND_PC; vacuolar protein sorting 45A;

KW leucocyte vacuolar protein sorting 45;
 KW vacuolar protein sorting 45B (yeast); VPS45A; H1; VPS45; VSP45; VPS45B;
 KW VPS54A; VSP45A; H1VPS45; vacuolar protein sorting 45A (yeast homolog);
 KW VPS54A; VPS45B; vacuolar protein sorting 45A (yeast), isoform CRA_a;
 KW vacuolar protein sorting 45A (yeast);
 KW vacuolar protein sorting 45 homolog (S. cerevisiae);
 KW vacuolar protein sorting 45 isoform; unnamed protein product; G05764;
 KW G05798; GO6886; GO6904; GO6954; GO16020; GO16192.
 XX
 OS Homo sapiens.

XX
 PN US2010151467-A1.

XX
 PD 17-JUN-2010.

XX
 PF 08-SEP-2009; 2009US-00584615.

XX
 PR 24-APR-2003; 2003WO-US012946.
 PR 22-JUL-2005; 2005US-00511937.

XX
 PA (XDXX-) XDX INC.

XX
 PI Fry K, Ly N, Morris M, Prentice J, Rosenberg S, Wohlgemuth J;
 PI Woodward R;

XX DR WPI; 2010-G86279/41.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX
 PT Diagnosing or monitoring transplant rejection comprises detecting the
 PT expression level of a nucleic acid in the patient to diagnose or monitor
 PT transplant rejection in the patient.

XX PS Example 1; SEQ ID NO 2612; 146pp; English.

CC The present invention relates to a method for diagnosing or monitoring
 CC transplant rejection, particularly cardiac transplant rejection in a
 CC patient. The method comprises detecting the expression level of a gene
 CC sequence preferably AYE11908 in a patient, by measuring the RNA level
 CC expressed by the gene sequence. AYE14212-AYE14438 are proteins encoded by
 CC gene expression markers AYE12145-AYE12476 for diagnosing and monitoring
 CC allograft rejection.

CC Revised record issued on 19-AUG-2010 : Enhanced with precomputed
 CC information from BOND.

XX SQ Sequence 570 AA;

```
Query Match          100.0%;  Score 2898;  DB 3;  Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||

Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||

Qy 61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYFIYFSNVISKSDVKS LAEADEQEVVVA 120
 |||||||

Db 61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYFIYFSNVISKSDVKS LAEADEQEVVVA 120
 |||||||

Qy 121 EVQEFGYGDYIAVNPHLFLSNI LGCCQGRNWDPQLSRTTQGLTALLLSLKCPMIRYQLS 180
 |||||||

Db 121 EVQEFGYGDYIAVNPHLFLSNI LGCCQGRNWDPQLSRTTQGLTALLLSLKCPMIRYQLS 180
 |||||||

Qy 181 SEAARKRLAEVCVKQVITKEYELFEEFRRTVEPPLLILDRCDDA1TPLLNQWTYQAMVHELL 240
 |||||||

Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEPPLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFNAEIGSNIKNLMEDFQKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSEAEDEFYANNMYLNFNAEIGSNIKNLMEDFQKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEKVR	420
Db	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEKVR	420
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Db	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLDRDPQDIIVFVIGGATYEALTVYNLNRTTPGVRIVLGTTVHN	540
Db	481	RLKENLYPYLGPSTLDRDPQDIIVFVIGGATYEALTVYNLNRTTPGVRIVLGTTVHN	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570

RESULT 9

ABB57217

ID ABB57217 standard; protein; 570 AA.

XX

AC ABB57217;

XX

DT 15-JUN-2007 (revised)
DT 07-MAR-2002 (first entry)

XX

DE Mouse ischaemic condition related protein sequence SEQ ID NO:527.

XX

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; BOND_PC;
KW vacuolar protein sorting 45;
KW vacuolar protein sorting-associated protein 45;
KW vacuolar protein sorting protein 45;
KW vacuolar protein sorting 45 [Mus musculus]; Vps45; mVps45; AI462172;
KW AWS54165; vacuolar protein sorting 45 (yeast);
KW Vacuolar protein sorting 45 (yeast) [Mus musculus];
KW vacuolar protein sorting homolog;
KW vacuolar protein sorting homolog [Mus musculus]; G05515; G06810; G06904;
KW G015031; G016020; G016192.

XX

OS Mus musculus.

XX

PN WO200188188-AZ.

XX

PD 22-NOV-2001.

XX

PF 18-MAY-2001; 2001WO-JP004192.

XX

PR 18-MAY-2000; 2000JP-00145977.

XX

PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX

PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX

DR WPI; 2002-034733/04.

DR N-PSDB; ABI99530.

DR PC:NCBI; gi7305631.

DR PC:SWISSPROT; P97390.
 DR PC:BIND; 261867.

XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.

XX
 PS Claim 2; Page 1446-1448; 2690pp; English.

CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI9912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI9913 and ABI9914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX
 SQ Sequence 570 AA;

Query Match 98.1%; Score 2844; DB 1; Length 570;
 Best Local Similarity 97.0%;
 Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMYVTQSEILQKEVYLFERIDSQNR 60
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMYVTQSEILQKEVYLFERIDSQNR 60

Qy 61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYIFIYFSNVISKSDVKS LAEADQE VVA 120
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 EIMKHLKAICFLRPTKENVEYLIQELRRPKYSIYIFIYFSNVISKSDVKS LAEADQE VVA 120

Qy 121 EVQEFGYGDYIAVNPHLFLSNIILGCCQGRNWDPAQLSRTTQGLTALLLSLKCPMIRYQLS 180
 |||||||:|||||:|||||:|||||:|||||:
 Db 121 EVQEFGYGDYIAVNPHLFLSNIILGCCQGRNWDPAQLSRTTQGLTALLLSLKCPMIRYQLS 180

Qy 181 SEAAKRLAECKVQVITKEYELFEFRRTEVPPLLLIDRCCDAITPLLNQWTYQAMVHELL 240
 |||||||:|||||:|||||:|||||:
 Db 181 SEAAKRLGECKVQVVISKEYELFEFRRTEVPPLLLIDRCCDAITPLLNQWTYQAMVHELL 240

Qy 241 GINNNRIDLSRVPGKISDKLREVVLSAENDEFYANNMYLNAEIGSNIKNL MEDFQKKPK 300
 |||||||:|||||:
 Db 241 GINNNRIDLSRVPGKISDKLREVVLSAENDEFYANNMYLNAEIGSNIKNL MEDFQKKPK 300

Qy 301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLLEVSE VEQELACQ 360
 |||||||:|||||:
 Db 301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLLEVSE VEQELACQ 360

Qy 361 NDHSSALQNIKRLLQNPKVTEFDAVLMLYALHYERHSSNLSPLGMLMDLRNKG VSEKYR 420
 |||||||:|||||:
 Db 361 NDHSSALQNVKRLLQNPKVTEFDAVLMLYALHYERHSSNLSPLGLIVDLRSKGVAEKYR 420

Qy 421 KLVSAVVEYGGKRVRGSDLFSPKD AVAITKQFLKGLKG VENVYTQHQPLHETLDH LIKG 480
 |||||||:
 Db 421 KLVSAVVEYGGKRVRGSDLFSPKD AVAITKQFLKGLKG VENVYTQHQPLHETLDH LIKG 480

Qy 481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALT VYLNRLRTPGVRIVLGTTVHN T 540

Db 481 RLKENLYPYLGPSTLRDRPQDIIVFIIGGATYEEALT VYLNRLTPGVRLGGTTIHNT 540
 Qy 541 KSFLEEVLASGLHSRSKES SQVTSRSASRR 570
 Db 541 KSFLEEVLASGLHSRSRESSQATSR SANRR 570

RESULT 10
 ADE61222
 ID ADE61222 standard; protein; 570 AA.

XX
 AC ADE61222;
 XX
 DT 15-JUN-2007 (revised)
 DT 29-JAN-2004 (first entry)
 XX

DE Rat Protein AAB53041, SEQ ID NO 7140.
 XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung;
 KW BOND_PC; vacuolar protein sorting 45; vesicular transport protein rvp45;
 KW vacuolar protein sorting 45 [Rattus norvegicus]; Vps45; Vsp45a; MGC;
 KW MGC93104; vacuolar protein sorting 45 (yeast);
 KW Vacuolar protein sorting 45 (yeast) [Rattus norvegicus]; rvp45;
 KW rvp45 [Rattus norvegicus]; GO5515; GO5764; GO5798; GO6886; GO6904;
 KW GO6954; GO15031; GO16020; GO16192.
 XX

OS Rattus norvegicus.
 XX

PN WO2003016475-A2.
 XX

PD 27-FEB-2003.
 XX

PF 14-AUG-2002; 2002WO-US025765.
 XX

PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX

PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX

PI Woolf C, D'urso D, Befort K, Costigan M;
 XX

DR WPI; 2003-268312/26.
 DR GENBANK; AAB53041.
 DR PC:NCBI; gi25742604.
 DR PC:SWISSPROT; 008700.
 XX

PT New composition comprising two or more isolated polypeptides, useful for
 preparing a medicament for treating pain in an animal.
 XX

PS Claim 1; Page; 1017pp; English.
 XX

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX

SQ Sequence 570 AA;

Query Match	98.0%	Score	2840	DB	1	Length	570;
Best Local Similarity	97.2%						
Matches	554	Conservative	12	Mismatches	4	Indels	0
Gaps	0						
Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60				
Db	1						
Qy	61	EIMKHLKAICFLRPTKENVDYIQQELRPRKYTIYIFIYSNVISKSDVKSLSAEADEQEVVAA	120				
Db	61						
Qy	121	EVQEFGYDGYIAVNPHLFLSLNILGCCQGRNWDPQAQLSRITQGLTALLLSKKCPMIRYQLS	180				
Db	121						
Qy	181	SEAARKRLAECVKQVITKEYLEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240				
Db	181						
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNAEIGSNIKNLMEDFQKKPK	300				
Db	241						
Qy	301	EQQKLESIADMKAFAVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360				
Db	301						
Qy	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMMDLRNKGVSEKyr	420				
Db	361						
Qy	421	KLVSAVEYGGKVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480				
Db	421						
Qy	481	KLKENLYPYLGSTLDRPQDIIVFVIGGATYYEALTVYNLNRTTPGVRIVLGGTTVHNT	540				
Db	481						
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570				
Db	541						

RESULT 11

ABG04478
 ID ABG04478 standard; protein; 578 AA.
 XX
 AC ABG04478;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #4469.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS68665.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 34837; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 578 AA;

Query Match 97.2%; Score 2815.5; DB 1; Length 578;
 Best Local Similarity 97.7%;
 Matches 558; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||||||

Db	8 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 67
Qy	61 EIMKHLKAICFLRPTKENVDYIIQELRPKYTIYFIYFSNVISKSDVKS LA-EADEQEVV 119 : :
Db	68 EIMKHLKAICFLRPTKENVDYIIQELRPKYTIYFIYFSNVISKSDVEIGLKLIEQEVV 127
Qy	120 AEVQE FYGDYIAVNPHFLSNI LGCCQGRNWDP AQLSRTT QGLT ALLLSLKCPMIRYQL 179 : :
Db	128 AEVQE FYGDYIAVNPHFLSNI LGCCQGRNWDP AQLSRTT QGLT ALLLSLKCPMIRYQL 187
Qy	180 SSEAKRLAECVKQVITKEYELFEPRRTEVPPLL LILDRCDDAITP LNLQWTYQAMVHEL 239 : :
Db	188 SSEAKRLAECVKQVITKEYELFEPRRTEVPPLL LILDRLDDAITP LNLQWTYQAMVHEL 247
Qy	240 LGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKP 299 : :
Db	248 LGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKP 307
Qy	300 KEQQKLESIADMKA FVENYPQFKKMSGT SKHVT VVGELSRLV SERNL LEVSE VEQELAC 359 : :
Db	308 KEQQKLESIGSMKA FVENYPQFKKMSGT SKHVT VVGELSRLV SERNL LEVSE VEQELAC 367
Qy	360 QNDHS SALQN IKR LLQNP KVT EFD AAR LVM LYAL HYER HSS NSL PGL MMD LRN KG VSE KY 419 : :
Db	368 QNDHS SALQN IKR LLQNP KVT EFD AAR LVM LYAL HYER HSS NSL PGL MMD LRN KG VSE KY 427
Qy	420 RKLVS AVVEYGGK RVRS GDSL FSPK DAVA ITK QFL KLG KGV NVT QHQ PFL HET LDH LIK 479 : :
Db	428 RKLVS AVVEYGGK RVRS GDSL FSPK DAVA ITK QFL KLG KGV NVT QHQ PFL HET LDH LIK 487
Qy	480 GRL KEN LY P YLGP ST LDRP QD II VFV IGG AT YEE AL T VY NLN RT PGV RIV LGG TT VHN 539 : :
Db	488 GRL KEN LY P YLGP ST LDRP QD II VFV IGG AT YEE AL T VY NLN RT PGV RIV LGG TT VHN 547
Qy	540 TKS FLEE VL AS GLH SR SK ESS SQV TS RS A SRR 570 : :
Db	548 TKS FLEE VL AS GLH SR SK ESS SQV TS RS A SRR 578

RESULT 12

AAO21766

ID AAO21766 standard; protein; 390 AA.

XX

AC AAO21766;

XX

DT 15-JUN-2007 (revised)

DT 13-SEP-2002 (first entry)

XX

DE Human ribosomal protein 42-9.

XX

KW Human ribosomal protein 42.9; protein metabolism disturbance disease;

KW DNA recombination; embryonic development deformity; tumour; BOND_PC;

KW vacuolar protein sorting 45A isoform;

KW vacuolar protein sorting 45A isoform [Homo sapiens]; GO5764; GO5798;

KW GO6886; GO6904; GO6954; GO16020; GO16192.

XX

OS Homo sapiens.

XX

PN CN1333254-A.

XX

PD 30-JAN-2002.

XX

PF 07-JUL-2000; 2000CN-00117043.

XX

PR 07-JUL-2000; 2000CN-00117043.

XX

PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.

SCORE Search Results Details for Application 09556178 and Search Result 20101203_114247_us-09-556-178-1.rup.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:52 ; Search time 347 Seconds
(without alignments)
6830.570 Million cell updates/sec

Title: US-09-556-178-1

Perfect score: 2898

Sequence: 1 MNVVFAVKQYISKMIEDSGP.....GLHRSRSKESSQVTSRSASRR 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 12869322 seqs, 4158259533 residues

Total number of hits satisfying chosen parameters: 12869322

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_201011:*

1: uniprot_sprot:*

2: uniprot_trembl:*

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	2898	100.0	570	1	VPS45_HUMAN		Q9nrw7 RecName: Fu
2	2898	100.0	570	2	D3DUZ9_HUMAN		D3duz9 SubName: Fu
3	2888	99.7	570	2	Q53FR8_HUMAN		Q53fr8 SubName: Fu
4	2868	99.0	570	2	D2HBV3_ATLME		D2hbv3 SubName: Fu
5	2864	98.8	570	2	A4FXU9_BOVIN		A4fxu9 SubName: Fu
6	2844	98.1	570	1	VPS45_MOUSE		P97390 RecName: Fu
7	2841	98.0	570	2	Q3THX4_MOUSE		Q3thx4 SubName: Fu
8	2840	98.0	570	1	VPS45_RAT		O08700 RecName: Fu
9	2716	93.7	534	2	B7Z360_XENAN		B7z360 SubName: Fu
10	2561	88.4	570	2	Q0D2D9_XENTR		Q0d2d9 SubName: Fu
11	2552	88.1	570	2	Q5XHB0_XENLA		Q5xhb0 SubName: Fu
12	2426	83.7	568	2	A8E7N5_DANRE		A8e7n5 SubName: Fu
13	2308	79.6	543	2	Q4TAW3_TETNG		Q4taw3 SubName: Fu
14	2244	77.4	445	2	B7Z5E4_HUMAN		B7z5e4 SubName: Fu
15	2164.5	74.7	538	2	B7Z5D4_HUMAN		B7z5d4 SubName: Fu
16	2129.5	73.5	571	2	C3Y1S4_BRAFL		C3y1s4 SubName: Fu
17	2128.5	73.4	434	2	B7Z1D7_HUMAN		B7z1j7 SubName: Fu
18	1971	68.0	568	2	A7S9U5_NEMVE		A7s9u5 SubName: Fu

19	1920	66.3	390	2	A0AR27_HUMAN	A0ar27 SubName: Fu
20	1764	60.9	377	2	Q5ZJG4_CHICK	Q5zjg4 SubName: Fu
21	1711.5	59.1	548	2	B3RRU0_TRIAD	B3rru0 SubName: Fu
22	1693.5	58.4	569	2	D7EHQ8_TRICA	D7ehq8 SubName: Fu
23	1587.5	54.8	574	2	B3NZQ1_DROER	B3nzb1 SubName: Fu
24	1584	54.7	574	2	B4PUQ8_DROYA	B4puq8 SubName: Fu
25	1584	54.7	574	2	Q9VHB5_DROME	Q9vhb5 SubName: Fu
26	1583	54.6	388	2	B5X429_SALSA	B5x429 SubName: Fu
27	1578.5	54.5	564	2	B4QWQ4_DROSI	B4qwq4 SubName: Fu
28	1577.5	54.4	574	2	B4JFE0_DROGR	B4jfe0 SubName: Fu
29	1576.5	54.4	574	2	B4M4B7_DROVI	B4m4b7 SubName: Fu
30	1574	54.3	574	2	B3M2G2_DROAN	B3m2g2 SubName: Fu
31	1569	54.1	574	2	Q295J1_DROPS	Q295j1 SubName: Fu
32	1562	53.9	574	2	B4NB39_DROWI	B4nb39 SubName: Fu
33	1560	53.8	575	2	D3TNU1_GLOMM	D3tnu1 SubName: Fu
34	1556.5	53.7	574	2	B4K664_DROMO	B4k664 SubName: Fu
35	1547.5	53.4	316	2	Q5T4Q0_HUMAN	Q5t4q0 SubName: Fu
36	1533	52.9	601	2	E0VVD5_PEDHC	E0vvd5 SubName: Fu
37	1524	52.6	574	2	Q7Q285_ANOGA	Q7q285 SubName: Fu
38	1493	51.5	574	2	Q17MG1_AEDAE	Q17mg1 SubName: Fu
39	1483.5	51.2	573	2	B0WJR0_CULQU	B0wjr0 SubName: Fu
40	1469	50.7	593	2	A6RJR5_BOTFB	A6rjr5 SubName: Fu
41	1468.5	50.7	593	2	C5P291_COCOP7	C5p291 SubName: Fu
42	1454.5	50.2	593	2	C4JP37_UNCRE	C4jp37 SubName: Fu
43	1449.5	50.0	549	2	B4HJY0_DROSE	B4hjy0 SubName: Fu
44	1443.5	49.8	593	2	C1GG11_PARBD	C1gg11 SubName: Fu
45	1441.5	49.7	553	2	A9UQW8_MONBE	A9uqw8 SubName: Fu

ALIGNMENTS

RESULT 1

VPS45_HUMAN

ID VPS45_HUMAN Reviewed; 570 AA.
 AC Q9NRN7; Q15715; Q5T4P6; Q9Y4Z6;
 DT 19-SEP-2002, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-2000, sequence version 1.
 DT 02-NOV-2010, entry version 81.
 DE RecName: Full=Vacuolar protein sorting-associated protein 45;
 DE Short=h-VPS45;
 DE Short=h1Vps45;
 GN Name=VPS45; Synonyms=VPS45A, VPS45B;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=97149272; PubMed=8996080; DOI=10.1016/S0378-1119(96)00367-8;
 RA Pevsner J., Hsu S.-C., Hyde P.S., Scheller R.H.;
 RT "Mammalian homologues of yeast vacuolar protein sorting (vps) genes
 RT implicated in Golgi-to-lysosome trafficking.";
 RL Gene 183:7-14(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Leukocyte;
 RX MEDLINE=99332720; PubMed=10404641; DOI=10.1016/S1357-2725(99)00017-5;
 RA Rajasekariah P., Eyre H.J., Stanley K.K., Walls R.S., Sutherland G.R.;
 RT "Molecular cloning and characterization of a cDNA encoding the human
 RT leucocyte vacuolar protein sorting (h1Vps45).";
 RL Int. J. Biochem. Cell Biol. 31:683-694(1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Hematopoietic stem cell;
 RA Gu J., Huang Q., Yu Y., Xu S., Han Z., Fu G., Zhou J., Wang Y.,
 RA Huang C., Ren S., Tu Y., Chen Z.;
 RT "Novel genes expressed in hematopoietic stem/progenitor cells from

RT myelodysplastic syndrome patients.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Seike M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirao S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotute T., Kusano J.,
 RA Kaneko K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=16710414; DOI=10.1038/nature04727;
 RA Gregory S.G., Barlow K.F., McLay K.E., Kaul R., Swarbreck D.,
 RA Dunham A., Scott C.E., Howe K.L., Woodfine K., Spencer C.C.A.,
 RA Jones M.C., Gillson C., Searle S., Zhou Y., Kokocinski F.,
 RA McDonald L., Evans R., Phillips K., Atkinson A., Cooper R., Jones C.,
 RA Hall R.E., Andrews T.D., Lloyd C., Ainscough R., Almeida J.P.,
 RA Ambrose K.D., Anderson F., Andrew R.W., Ashwell R.I.S., Aubin K.,
 RA Babbage A.K., Baggaley C.L., Bailey J., Beasley H., Bethel G.,
 RA Bird C.P., Bray-Allen S., Brown J.Y., Brown A.J., Buckley D.,
 RA Burton J., Bye J., Carder C., Chapman J.C., Clark S.Y., Clarke G.,
 RA Clee C., Cobley V., Collier R.E., Corby N., Coville G.J., Davies J.,
 RA Deadman R., Dunn M., Earthrow M., Ellington A.G., Errington H.,
 RA Frankish A., Frankland J., French L., Garner P., Garnett J., Gay L.,
 RA Ghori M.R.J., Gibson R., Gilby L.M., Gillett W., Glithero R.J.,
 RA Graham D.V., Griffiths C., Griffiths-Jones S., Grocock R.,
 RA Hammond S., Harrison E.S.I., Hart E., Haugen E., Heath P.D.,
 RA Holmes S., Holt K., Howden P.J., Hunt A.R., Hunt S.E., Hunter G.,
 RA Isherwood J., James R., Johnson C., Johnson D., Joy A., Kay M.,
 RA Kershaw J.K., Kibukawa M., Kimberley A.M., King A., Knights A.J.,
 RA Lad H., Laird G., Lawlor S., Leongamornlert D.A., Lloyd D.M.,
 RA Loveland J., Lovell J., Lush M.J., Lyne R., Martin S.,
 RA Mashreghi-Mohammadi M., Matthews L., Matthews N.S.W., McLaren S.,
 RA Milne S., Mistri S., Moore M.J.F., Nickerson T., O'Dell C.N.,
 RA Oliver K., Palmeira A., Palmer S.A., Parker A., Patel D., Pearce A.V.,
 RA Peck A.I., Pelan S., Phelps K., Phillimore B.J., Plumb R., Rajan J.,
 RA Raymond C., Rouse G., Saenphimmachak C., Sehra H.K., Sheridan E.,
 RA Shownkeen R., Sims S., Skuce C.D., Smith M., Steward C.,
 RA Subramanian S., Sycamore N., Tracey A., Tromans A., Van Helmond Z.,
 RA Wall M., Wallis J.M., White S., Whitehead S.L., Wilkinson J.E.,
 RA Willey D.L., Williams H., Wilming L., Wray P.W., Wu Z., Coulson A.,
 RA Vaudin M., Sulston J.E., Durbin R.M., Hubbard T., Wooster R.,
 RA Dunham I., Carter N.P., McVean G., Ross M.T., Harrow J., Olson M.V.,

RA Beck S., Rogers J., Bentley D.R.;
 RT "The DNA sequence and biological annotation of human chromosome 1.";
 RL Nature 441:315-321(2006).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Mural R.J., Istrail S., Sutton G.G., Florea L., Halpern A.L.,
 RA Mobarry C.M., Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R.,
 RA Flanigan M.J., Edwards N.J., Bolanos R., Fasulo D., Halldorsson B.V.,
 RA Hannenhalli S., Turner R., Yoosoph S., Lu F., Nusskern D.R.,
 RA Shue B.C., Zheng X.H., Zhong F., Delcher A.L., Huson D.H.,
 RA Kravitz S.A., Mouchard L., Reinert K., Remington K.A., Clark A.G.,
 RA Waterman M.S., Eichler E.E., Adams M.D., Hunkapiller M.W., Myers E.W.,
 RA Venter J.C.;
 RL Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Colon, and Hippocampus;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 RN [8]
 RP INTERACTION WITH ZFYVE20.
 RX MEDLINE=20517446; PubMed=11062261; DOI=10.1083/jcb.151.3.601;
 RA Nielsen E., Christoforidis S., Uttenweiler-Joseph S., Miaczynska M.,
 RA Dewitte F., Wilm M., Hoflack B., Zerial M.;
 RT "Rabenosyn-5, a novel Rab5 effector, is complexed with hVPS45 and
 recruited to endosomes through a FYVE finger domain.";
 RL J. Cell Biol. 151:601-612(2000).
 RN [9]
 RP INTERACTION WITH ZFYVE20.
 RX PubMed=11788822; DOI=10.1038/ngb744;
 RA de Renzis S., Soenrichsen B., Zerial M.;
 RT "Divalent Rab effectors regulate the sub-compartmental organization
 and sorting of early endosomes.";
 RL Nat. Cell Biol. 4:124-133(2002).
 RN [10]
 RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
 RA Colinge J., Superti-Furga G., Bennett K.L.;
 RL Submitted (OCT-2008) to UniProtKB.
 CC -!- FUNCTION: May play a role in vesicle-mediated protein trafficking
 CC from the Golgi stack through the trans-Golgi network.
 CC -!- SUBUNIT: Interacts with STX6 (By similarity). Interacts with
 CC ZFYVE20.
 CC -!- SUBCELLULAR LOCATION: Golgi apparatus membrane; Peripheral
 CC membrane protein (By similarity). Endosome membrane; Peripheral
 CC membrane protein (By similarity). Note=Associated with
 CC Golgi/endosomal vesicles and the trans-Golgi network (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: Ubiquitous. Expression was highest in testis,
 CC heart and brain, intermediate in kidney, spleen, prostate, ovary,
 CC small intestine and thymus and low in lung, skeletal muscle,
 CC placenta, colon, pancreas, peripheral blood leukocytes and liver.
 CC -!- SIMILARITY: Belongs to the STXBP/unc-18/SEC1 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; U35246; AAC50931.1; -; mRNA.
 DR EMBL; AJ133421; CAB40417.1; -; mRNA.
 DR EMBL; AF165513; AAF86643.1; -; mRNA.
 DR EMBL; AK023170; BAB14443.1; -; mRNA.
 DR EMBL; AL358073; CAI14265.1; -; Genomic_DNA.
 DR EMBL; CH471121; EAW53584.1; -; Genomic_DNA.
 DR EMBL; BC012932; AAH12932.1; -; mRNA.
 DR EMBL; BC028382; AAH28382.1; -; mRNA.
 DR IPI; IPI00090327; -.
 DR PIR; JC5722; JC5722.
 DR RefSeq; NP_009190.2; -.

DR UniGene; Hs.443750; -.
 DR ProteinModelPortal; Q9NRW7; -.
 DR SMR; Q9NRW7; 6-548.
 DR STRING; Q9NRW7; -.
 DR PRIDE; Q9NRW7; -.
 DR Ensembl; ENST00000369130; ENSP00000358126; ENSG00000136631.
 DR GeneID; 11311; -.
 DR KEGG; hsa:11311; -.
 DR UCSC; uc00letp.1; human.
 DR CTD; 11311; -.
 DR GeneCards; GC01P150039; -.
 DR H-InvDB; HIX0199801; -.
 DR HGNC; HGNC:14579; VPS45.
 DR HPA; HPA027425; -.
 DR HPA; HPA027441; -.
 DR MIM; 610035; gene.
 DR PharmGKB; PA37901; -.
 DR HOGENOM; HBG559243; -.
 DR HOVERGEN; HBG059810; -.
 DR InParanoid; Q9NRW7; -.
 DR OMA; GTIIHNT; -.
 DR OrthoDB; EOG9PCDBM; -.
 DR PhylomeDB; Q9NRW7; -.
 DR NextBio; 42971; -

Query Match 100.0%; Score 2898; DB 1; Length 570;
 Best Local Similarity 100.0%
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MNVVF AVKQYI SKMIED SGPM KVLLMDKETTGIVS MVYTQSEILQ KEVYL FERIDS QNR 60
Db	1 MNVVF AVKQYI SKMIED SGPM KVLLMDKETTGIVS MVYTQSEILQ KEVYL FERIDS QNR 60
Qy	61 EIMKHLKAICFLRPTKENV D YI QELRRPKY T IYI FYSNVISKS DVKS L A EAD E QEVVA 120
Db	61 EIMKHLKAICFLRPTKENV D YI QELRRPKY T IYI FYSNVISKS DVKS L A EAD E QEVVA 120
Qy	121 EVQE FYGDYIA VNPHL FS LN ILG C C Q GRN WD PA QLS RIT T QGL T ALL L S L K K C P M I R Y Q L S 180
Db	121 EVQE FYGDYIA VNPHL FS LN ILG C C Q GRN WD PA QLS RIT T QGL T ALL L S L K K C P M I R Y Q L S 180
Qy	181 SEAAK RL AECV K QV IT KEY E L F E F R R T E V V P L L L I I D R C D D A I T P L L N Q W T Y Q A M V H E L L 240
Db	181 SEAAK RL AECV K QV IT KEY E L F E F R R T E V V P L L L I I D R C D D A I T P L L N Q W T Y Q A M V H E L L 240
Qy	241 G I N N N R I D L S R V P G I S K D L R E V V L S A E N D E F Y A N N M Y L N F A E I G S N I K N L M E D F Q K K P K 300
Db	241 G I N N N R I D L S R V P G I S K D L R E V V L S A E N D E F Y A N N M Y L N F A E I G S N I K N L M E D F Q K K P K 300
Qy	301 E QQK L E S I A D M K A F V E N Y P Q F K K M S G T V S K H V T V V G E L S R L V S E R N L L E V S E V E Q E L A C Q 360
Db	301 E QQK L E S I A D M K A F V E N Y P Q F K K M S G T V S K H V T V V G E L S R L V S E R N L L E V S E V E Q E L A C Q 360
Qy	361 N D H S S A L Q N I K R L L Q N P K V T E F D A A R L V M L Y A L H Y E R H S S N S L P G L M M D L R N K G V S E K Y R 420
Db	361 N D H S S A L Q N I K R L L Q N P K V T E F D A A R L V M L Y A L H Y E R H S S N S L P G L M M D L R N K G V S E K Y R 420
Qy	421 K L V S A V V E Y G G K R V R G S D L F S P K D A V A I T K Q F L K L G K G V E N V Y T Q H Q P F L H E T L D H L I K G 480
Db	421 K L V S A V V E Y G G K R V R G S D L F S P K D A V A I T K Q F L K L G K G V E N V Y T Q H Q P F L H E T L D H L I K G 480
Qy	481 R L K E N L Y P Y L G P S T L R D R P Q D I I V F V I G G A T Y E E A L T V Y N L N R T T P G V R I V L G G T T V H N T 540
Db	481 R L K E N L Y P Y L G P S T L R D R P Q D I I V F V I G G A T Y E E A L T V Y N L N R T T P G V R I V L G G T T V H N T 540
Qy	541 K S F L E E V L A S G L H S R S K E S S Q V T S R S A S R R 570
Db	541 K S F L E E V L A S G L H S R S K E S S Q V T S R S A S R R 570

RESULT 2
D3DUZ9_HUMAN
ID D3DUZ9_HUMAN Unreviewed; 570 AA.
AC D3DUZ9;
DT 23-MAR-2010, integrated into UniProtKB/TrEMBL.
DT 23-MAR-2010, sequence version 1.
DT 02-NOV-2010, entry version 8.
DE SubName: Full=Vacuolar protein sorting 45A (Yeast), isoform CRA_a;
GN Name=VPS45A; ORFNames=hCG_39383;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21108353; PubMed=11181995; DOI=10.1126/science.1058040;
RA Venter J.C., Adams M.D., Myers E.W., Li P.W., Mural R.J., Sutton G.G.,
RA Smith H.O., Yandell M., Evans C.A., Holt R.A., Gocayne J.D.,
RA Amanatides P., Ballew R.M., Huson D.H., Wortman J.R., Zhang Q.,
RA Kodira C.D., Zheng X.H., Chen L., Skupski M., Subramanian G.,
RA Thomas P.D., Zhang J., Gabor Miklos G.L., Nelson C., Broder S.,
RA Clark A.G., Nadeau J., McKusick V.A., Zinder N., Levine A.J.,
RA Roberts R.J., Simon M., Slayman C., Hunkapiller M., Bolanos R.,
RA Delcher A., Dew I., Fasulo D., Flanigan M., Florea L., Halpern A.,
RA Hannenhalli S., Kravitz S., Levy S., Mobarry C., Reinert K.,
RA Remington K., Abu-Threideh J., Beasley E., Biddick K., Bonazzi V.,
RA Brandon R., Cargill M., Chandramouliwaran I., Charlton R.,
RA Chaturvedi K., Deng Z., Di Francesco V., Dunn P., Eilbeck K.,
RA Evangelista C., Gabrielson A.E., Gan W., Ge W., Gong F., Gu Z.,
RA Guan P., Heiman T.J., Higgins M.E., Ji R.R., Ke Z., Ketchum K.A.,
RA Lai Z., Lei Y., Li Z., Li J., Liang Y., Lin X., Lu F., Merkulov G.V.,
RA Milshina N., Moore H.M., Naik A.K., Narayan V.A., Neelam B.,
RA Nusskern D., Rusch D.B., Salzberg S., Shao W., Shue B., Sun J.,
RA Wang Z., Wang A., Wang X., Wang J., Wei M., Wides R., Xiao C., Yan C.,
RA Yao A., Ye J., Zhan M., Zhang W., Zhang H., Zhao Q., Zheng L.,
RA Zhong F., Zhong W., Zhu S., Zhao S., Gilbert D., Baumhueter S.,
RA Spier G., Carter C., Cravchik A., Woodage T., Ali F., An H., Awe A.,
RA Baldwin D., Baden H., Barnstead M., Barrow I., Beeson K., Busam D.,
RA Carver A., Center A., Cheng M.L., Curry L., Danaher S., Davenport L.,
RA Desilets R., Dietz S., Dodson K., Doup L., Ferriera S., Garg N.,
RA Gluecksmann A., Hart B., Haynes J., Haynes C., Heiner C., Hladun S.,
RA Hostin D., Houck J., Howland T., Ibeagwam C., Johnson J., Kalush F.,
RA Kline L., Koduru S., Love A., Mann F., May D., McCawley S.,
RA McIntosh T., McMullen I., Moy M., Moy L., Murphy B., Nelson K.,
RA Pfannkoch C., Pratts E., Puri V., Qureshi H., Reardon M.,
RA Rodriguez R., Rogers Y.H., Romblad D., Ruhfel B., Scott R., Sitter C.,
RA Smallwood M., Stewart E., Strong R., Sub E., Thomas R., Tint N.N.,
RA Tse S., Vech C., Wang G., Wetter J., Williams S., Williams M.,
RA Windsor S., Winn-Denn E., Wolfe K., Zaveri J., Zaveri K., Abril J.F.,
RA Guigo R., Campbell M.J., Sjolander K.V., Karlak B., Kejariwal A.,
RA Mi H., Lazareva B., Hatton T., Narechania A., Diemer K.,
RA Muruganujan A., Guo N., Sato S., Bafna V., Istrail S., Lippert R.,
RA Schwartz R., Walenz B., Yoosoph S., Allen D., Basu A., Baxendale J.,
RA Blick L., Caminha M., Carnes-Stine J., Caulk P., Chiang Y.H.,
RA Coyne M., Dahlke C., Mays A., Dombroski M., Donnelly M., Ely D.,
RA Esparham S., Fosler C., Gire H., Glnaski S., Glasser K., Glodek A.,
RA Gorokhov M., Graham K., Groisman B., Harris M., Heil J., Henderson S.,
RA Hoover J., Jennings D., Jordan C., Jordan J., Kasha J., Kagan L.,
RA Kraft C., Levitsky A., Lewis M., Liu X., Lopez J., Ma D., Majoros W.,
RA McDaniel J., Murphy S., Newman M., Nguyen T., Nguyen N., Nodell M.,
RA Pan S., Peck J., Peterson M., Rowe W., Sanders R., Scott J.,
RA Simpson M., Smith T., Sprague A., Stockwell T., Turner R., Venter E.,
RA Wang M., Wen M., Wu M., Xia A., Zandieh A., Zhu X.;
RT "The sequence of the human genome.";
RL Science 291:1304-1351(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Mural R.J., Istrail S., Sutton G., Florea L., Halpern A.L.,
RA Mobarry C.M., Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R.,

RA Flanigan M.J., Edwards N.J., Bolanos R., Fasulo D., Halldorsson B.V.,
 RA Hannenhalli S., Turner R., Yoosoph S., Lu F., Nusskern D.R.,
 RA Shue B.C., Zheng X.H., Zhong F., Delcher A.L., Huson D.H.,
 RA Kravitz S.A., Moucharad L., Reinert K., Remington K.A., Clark A.G.,
 RA Waterman M.S., Eichler E.E., Adams M.D., Hunkapiller M.W., Myers E.W.,
 RA Venter J.C.;
 RL Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
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 CC
 DR EMBL; CH471121; EAN53585.1; -; Genomic_DNA.
 DR IPI; IPI00090327; -.
 DR RefSeq; NP_009190.2; -.
 DR UniGene; Hs.443750; -.
 DR ProteinModelPortal; D3DUZ9; -.
 DR SMP; D3DUZ9; 2-129.
 DR Ensembl; ENST00000369130; ENSP00000358126; ENSG00000136631.
 DR GeneID; 11311; -.
 DR KEGG; hsa:11311; -.
 DR CTD; 11311; -.
 DR HGNC; HGNC:14579; VPS45.
 DR GO; GO:0006904; Pivesicle docking involved in exocytosis; IEA:InterPro.
 DR InterPro; IPR001619; Sec1-like.
 DR PANTHER; PTHR11679; Sec1-like; 1.
 DR Pfam; PF00995; Sec1; 1.
 DR SUPFAM; SSF56815; Sec1-like; 1.
 PE 4: Predicted;
 SQ SEQUENCE 570 AA; 65077 MW; 5574F0BE3A7D4EB3 CRC64;

Query Match 100.0%; Score 2898; DB 2; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQNR 60
 |||||||
 Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQNR 60
 |||||||
 Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIFIYFSNVISKSDVKS LAEADEQEVVAA 120
 |||||||
 Db 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIFIYFSNVISKSDVKS LAEADEQEVVAA 120
 |||||||
 Qy 121 EVQEFYGYDIYAVNPFLS NLIGCCQGRNWDPAQLSRTIQGLTALLLSLKCPMIRYQLS 180
 |||||||
 Db 121 EVQEFYGYDIYAVNPFLS NLIGCCQGRNWDPAQLSRTIQGLTALLLSLKCPMIRYQLS 180
 |||||||
 Qy 181 SEAARKLAECKVQKVITKEYELFEFRTEVPPLLL ILDRCDDAITPLLNQWTYQAMVHELL 240
 |||||||
 Db 181 SEAARKLAECKVQKVITKEYELFEFRTEVPPLLL ILDRCDDAITPLLNQWTYQAMVHELL 240
 |||||||
 Qy 241 GINNNRIDLRSVPGISKDLREVVLSAENDEFYANNMLNFAEIGSNIKNL MEDFQKKPK 300
 |||||||
 Db 241 GINNNRIDLRSVPGISKDLREVVLSAENDEFYANNMLNFAEIGSNIKNL MEDFQKKPK 300
 |||||||
 Qy 301 EQQKLESIADMKA FVENY PQFKKMSGTVS KVHTVV GELSRLV SERNL LEVSEVEQELACQ 360
 |||||||
 Db 301 EQQKLESIADMKA FVENY PQFKKMSGTVS KVHTVV GELSRLV SERNL LEVSEVEQELACQ 360
 |||||||
 Qy 361 NDHSSALQNIKRLQNPKVTEF DAARLVM LYALHYERHSSNSLPGLMMMDLRNKGVSEK YR 420
 |||||||
 Db 361 NDHSSALQNIKRLQNPKVTEF DAARLVM LYALHYERHSSNSLPGLMMMDLRNKGVSEK YR 420
 |||||||
 Qy 421 KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKG LKG VENVYTQHQPF LHETLDHLIKG 480
 |||||||
 Db 421 KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKG LKG VENVYTQHQPF LHETLDHLIKG 480
 |||||||
 Qy 481 RLKENLYPYLGPSTLDRDPQDIIVFVIGGATYEEALTVYLNRLTPGV RIVLGGTTVHNT 540
 |||||||
 Db 481 RLKENLYPYLGPSTLDRDPQDIIVFVIGGATYEEALTVYLNRLTPGV RIVLGGTTVHNT 540

Qy 541 KSFLEEVLASGLHRSRKESSQVTSRSASR 570
 |||||||
 Db 541 KSFLEEVLASGLHRSRKESSQVTSRSASR 570

RESULT 3
 Q53FR8_HUMAN
 ID Q53FR8_HUMAN Unreviewed; 570 AA.
 AC Q53FR8;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 05-OCT-2010, entry version 30.
 DE SubName: Full=Vacuolar protein sorting 45A variant;
 DE Flags: Fragment;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Stomach mucosa;
 RX MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
 RA Maruyama K., Sugano S.;
 RT "Oligo-capping: a simple method to replace the cap structure of
 eukaryotic mRNAs with oligoribonucleotides.";
 RL Gene 138:171-174(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Stomach mucosa;
 RX MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
 RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
 RT "Construction and characterization of a full length-enriched and a 5'-
 end-enriched cDNA library.";
 RL Gene 200:149-156(1997).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Stomach mucosa;
 RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
 RA Tanaka A., Yokoyama S.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AK223214; BAD96934.1; -; mRNA.
 DR IPI; IPI00090327; -.
 DR UniGene; Hs.443750; -.
 DR STRING; Q53FR8; -.
 DR PhosphoSite; Q53FR8; -.
 DR Ensembl; ENST00000369130; ENSP00000358126; ENSG00000136631.
 DR HGNC; HGNC:14579; VPS45.
 DR HOVERGEN; HBG059810; -.
 DR ArrayExpress; Q53FR8; -.
 DR Bgee; Q53FR8; -.
 DR GO; GO:0006949; Pivesicle docking involved in exocytosis; IEA:InterPro.
 DR InterPro; IPR001619; Sec1-like.
 DR PANTHER; PTHR11679; Sec1-like; 1.
 DR Pfam; PF00995; Sec1; 1.
 DR SUPFAM; SSF56815; Sec1-like; 1.
 PE 2: Evidence at transcript level;
 FT NON_TER 1 1
 SQ SEQUENCE 570 AA; 65070 MW; AD7733351ECEB551 CRC64;

Query Match 99.7%; Score 2888; DB 2; Length 570;
 Best Local Similarity 99.6%;
 Matches 568; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Gaps 0
 Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQRN 60
 |||||||

Db	1 MNVVFAVKQYISKMIEDSGPMKVLLMDKETTGVSMVTQSEILQKEVYLFERIDSQRN 60
Qy	61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYIYFIYFSNVISKS DVKSLAEADEQE VVA 120
Db	61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYIYFIYFSNVISKS DVKSLAEADEQE VVA 120
Qy	121 EVQEYFQGYDIAVNPHLFSNLIGCCQGRNWDPQLSRTTQGLTALLLSLKKCPMIRYQLS 180
Db	121 EVQEYFQGYDIAVNPHLFSNLIGCCQGRNWDPQLSRTTQGLAALLLSLKKCPMIRYQLS 180
Qy	181 SEAAKRLAE CVKQVITKEYELFEFRTEVPPLLLIDRCDDAITPLLNQWTYQAMVHELL 240
Db	181 SEAAKRLAE CVKQVITKEYELFEFRTEVPPLLLIDRCDDAITPLLNQWTYQAMVHELL 240
Qy	241 GINNNRIDL S RVP GISKDLR REVVL S AENDEF YANN MYL NFAE IGSNI KNL MED FQKKPK 300
Db	241 GINNNRIDL S RVP GISKDLR REVVL S AENDEF YANN MYL NFAE IGSNI KNL MED FQKKPK 300
Qy	301 EQQKLESIADMKA FVENYPQFKMSGTVKHVTVVGELSRLV SERN LLEVSEVEQELACQ 360
Db	301 EQQKLESIADMKA FVENYPQFKMSGTVKHVTVVGELSRLV SERN LLEVSEVEQELACQ 360
Qy	361 NDHSSALQNIKRLL QNP KVT EFD AARL VML YALHYER HSSN SLPGLMM DLRNKG VSEK YR 420
Db	361 NDHSSALQNIKRLL QNP KVT EFD AARL VML YALHYER HSSN SLPGLMM DLRNKG VSEK YR 420
Qy	421 KL VSAVVEYGGKRV RGS DL FSP KDAVAITKQFLKG LKG VEN VYTQHQPFLHETLDH LIKG 480
Db	421 KL VSAVVEYGGKRV RGS DL FSP KDAVAITKQFLKG LKG VEN VYTQHQPFLHETLDH LIKG 480
Qy	481 RL KLEN LY PLY LGP STL RD RP QDIIVF VIGGAT YEE ALTV YN LN RT PGV RIV LG GTT VHN T 540
Db	481 RL KLEN LY PLY LGP STL RD RP QDIIVF VIGGAT YEE ALTV YN LN RT PGV RIV LG GTT VHN T 540
Qy	541 KSFLEEVLASGLH SRS KESS QVT SR SAS R 570
Db	541 KSFLEEVLASGLH SRS KESS QVT SR SAS R 570

RESULT 4
D2HBV3_AILME

ID D2HBV3_AILME Unreviewed; 570 AA.
 AC D2HBV3;
 DT 09-FEB-2010, integrated into UniProtKB/TrEMBL.
 DT 09-FEB-2010, sequence version 1.
 DT 05-OCT-2010, entry version 6.
 DE SubName: Full=Putative uncharacterized protein;
 DE Flags: Fragment;
 GN ORFNames=PANDA_008031;
 OS Ailuropoda melanoleuca (Giant panda).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Ursidae;
 OC Ailuropoda.
 OX NCBI_TaxID=9646;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=20010809; DOI=10.1038/nature08696;
 RA Li R., Fan W., Tian G., Zhu H., He L., Cai J., Huang Q., Cai Q.,
 RA Li B., Bai Y., Zhang Z., Zhang Y., Wang W., Li J., Wei F., Li H.,
 RA Jian M., Li J., Zhang Z., Nielsen R., Li D., Gu W., Yang Z., Xuan Z.,
 RA Ryder O.A., Leung F.C., Zhou Y., Cao J., Sun X., Fu Y., Fang X.,
 RA Guo X., Wang B., Hou R., Shen F., Mu B., Ni P., Lin R., Qian W.,
 RA Wang G., Yu C., Nie W., Wang J., Wu Z., Liang H., Min J., Wu Q.,
 RA Cheng S., Ruan J., Wang M., Shi Z., Wen M., Liu B., Ren X., Zheng H.,
 RA Dong D., Cook K., Shan G., Zhang H., Kosiol C., Xie X., Lu Z.,
 RA Zheng H., Li Y., Steiner C.C., Lam T.T., Lin S., Zhang Q., Li G.,
 RA Tian J., Gong T., Liu H., Zhang D., Fang L., Ye C., Zhang J., Hu W.,
 RA Xu A., Ren Y., Zhang G., Bruford M.W., Li Q., Ma L., Guo Y., An N.,
 RA Hu Y., Zheng Y., Shi Y., Li Z., Liu Q., Chen Y., Zhao J., Qu N.,
 RA Zhao S., Tian F., Wang X., Wang H., Xu L., Liu X., Vinar T., Wang Y.,

RA Lam T.W., Yiu S.M., Liu S., Zhang H., Li D., Huang Y., Wang X.,
 RA Yang G., Jiang Z., Wang J., Qin N., Li L., Li J., Bolund L.,
 RA Kristiansen K., Wong G.K., Olson M., Zhang X., Li S., Yang H.,
 RA Wang J., Wang J.;
 RT "The sequence and de novo assembly of the giant panda genome.";
 RL Nature 463:311-317(2010).

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DR EMBL; GLI92667; EFB28489.1; -; Genomic_DNA.
 DR RefSeq; XP_002919362.1; -.
 DR GeneID; 100471437; -.
 DR GO; GO:0006904; Pivesicle docking involved in exocytosis; IEA:InterPro.
 DR InterPro; IPR001619; Secl-like.
 DR PANTHER; PTHR11679; Secl-like; 1.
 DR Pfam; PF00995; Secl; 1.
 DR SUPFAM; SSF56815; Secl-like; 1.
 PE 4: Predicted;
 FT NON_TER 570 570
 SQ SEQUENCE 570 AA; 65066 MW; F8E11EA1E1372D39 CRC64;

Query Match 99.0%; Score 2868; DB 2; Length 570;
 Best Local Similarity 98.1%;
 Matches 559; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNVVF AVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
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Db 1 MNVVF AVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQREVYLFERIDSQRN 60

Qy 61 EIMKHLKAICFLRPTKENVDYIQLRRPKTYIIFYFSNVISKSDVKS LAEADEQE VVA 120
 |||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||

Db 61 EIMKHLKAICFLRPTKENVDYIQLRRPKYSIYIFIYFSNVISKSDVKS LAEADEQE VVA 120

Qy 121 EVQE FYG DYIAVNPHL FS LN ILGC C QGRN WDPA QLS RIT QGLT ALL LSLKKC P MIR YQLS 180
 |||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||

Db 121 EVQE FYG DYIAVNPHL FS LS ILGC C QGRN WDPA QLS RIT QGLT ALL LSLKKC P MIR YQLS 180

Qy 181 SEA AKRLAECV KQV IT KEY ELY FE FRR TE VPP PLL LIDRC DDA IT PLLN QWT YQAMV HELL 240
 |||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||

Db 181 SEA AKRLAECV KQV IT KEY ELY FE FRR TE VPP PLL LIDRC DDA IT PLLN QWT YQAMV HELL 240

Qy 241 GI NN RIDL SRV PG ISK DL RVE VLS A ENDEF YAN NM YLN FA EIGS NI KNL MEDF QKK KP 300
 |||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||

Db 241 GI NN RIDL SRV PG ISK DL RVE VLS A ENDEF YAN NM YLN FA EIGS NI KNL MEDF QKK KP 300

Qy 301 EQ QK LE SIADM KAF VEN Y PQFK KM SGTV SKH TVV GEL SRL V SER NL LEV SE VE QEL ACQ 360
 |||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||

Db 301 EQ QK LE SIADM KAF VEN Y PQFK KM SGTV SKH TVV GEL SRL V SER NL LEV SE VE QEL ACQ 360

Qy 361 NDHSS AL QN I K R LL QN PK VTE F DA AR L VML Y AL HYER HSS NSL P GL MM D L R NK GV SE KYR 420
 |||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||

Db 361 NDHSS AL QN V K R LL QN PK VTE F DA TR L VML Y AL HYER HSS NSL P GL MM D L R NK GV SE KYR 420

Qy 421 KL VSA VVE YGG KRV RG SD LF SPK DAVA IT KQ FL KLG KGV EN VY TQH QPFL HET LDH LIKG 480
 |||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||

Db 421 KL VSA VVE YGG KRV RG SD LF SPK DAVA IT KQ FL KLG KGV EN VY TQH QPFL HET LDH LIKG 480

Qy 481 RL KEN LY P Y LG P ST LR DR P QD I IV FV I GGA T YEE AL T VY N L N RT T PG V R I VL GG TT V HNT 540
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||

Db 481 RL KEN LY P Y LG P ST LR DR P QD I IV FV I GGA T YEE AL T VY N L N RT T PG V R I VL GG TT V HNT 540

Qy 541 KSF LEE VLA SGL H LRS KESS QVT SRS ASR R 570
 |||||||:||||:||||:||||:||||:||||:|||

Db 541 KSF LEE VLA SGL H LRS R S S QVT SRS ASR R 570

RESULT 5

A4FX9_BOVIN

ID A4FX9_BOVIN

Unreviewed; 570 AA.

AC A4FUX9;
DT 17-APR-2007, integrated into UniProtKB/TrEMBL.
DT 17-APR-2007, sequence version 1.
DT 05-OCT-2010, entry version 19.
DE SubName: Full=VPS45 protein;
GN Name=VPS45;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=L1 Hereford; TISSUE=Thalamus;
RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL Submitted (SEP-2006) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; BC123422; AA123423.1; -; mRNA.
DR IPI; IPI00718070; -.
DR RefSeq; NP_001076970.1; -.
DR UniGene; Bt.13692; -.
DR ProteinModelPortal; A4FUX9; -.
DR STRING; A4FUX9; -.
DR Ensembl; ENSBTAT00000027499; ENSBTAP00000027499; ENSBTAG00000020635.
DR GeneID; 541230; -.
DR KEGG; bta:541230; -.
DR CTD; 541230; -.
DR eggNOG; maNOG05713; -.
DR HOVERGEN; HBG059810; -.
DR InParanoid; A4FUX9; -.
DR PhylomeDB; A4FUX9; -.
DR GO; GO:0006904; Pivesicle docking involved in exocytosis; IEA:InterPro.
DR InterPro; IPR001619; Sec1-like.
DR PANTHER; PTHR11679; Sec1-like; 1.
DR Pfam; PF00995; Sec1; 1.
DR SUPFAM; SSF56815; Sec1-like; 1.
PE 2: Evidence at transcript level;
SQ SEQUENCE 570 AA; 65136 MN; 7D976D91DA92A4F2 CRC64;

Query Match 98.8%; Score 2864; DB 2; Length 570;
Best Local Similarity 98.1%
Matches 559; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
Qy	61 EIMKHLKAICFLRPTEKVENDVYIQLERPKYTIYIFIYFSNVISKSVDVKS LAEADEQEVVAA 120
Db	61 EIMKHLKAICFLRPTEKVENDVYIQLERPKYTIYIFIYFSNVISKSVDVKS LAEADEQEVVAA 120
Qy	121 EVQEYFGDYIAVNPHLFSLNILGCCQGRNWDPQAQLSRTITQGLTALLLSLKCPMIRYQLS 180
Db	121 EVQEYFGDYIAVNPHLFSLNILGCCQGRNWDPVQLSRTITQGLTALLLSLKCPMIRYQLS 180
Qy	181 SEAARKLAECKVQVITKEYELFEFRTEVPLLLILDRCDADITPLNQWTYQAMVHELL 240
Db	181 SEAARKLAECKVQVITKEYELFEFRTEVPLLLILDRCDADITPLNQWTYQAMVHELL 240
Qy	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMLNFAEIGSNIKNLMEDFQKKKP 300
Db	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMLNFAEIGSNIKNLMEDFQKKKP 300

Qy	301	EQQQKLESIADMKAFFENYQPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Db	301	EQQQKLESIADMKAFFENYQPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNVKRRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMMDLRNKGVSEKYR	420
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKDAVIAITKQFLKGKGKVENVYTQHQPLHETLDHLIKG	480
Db	421	KLVSAVVEYGGKRVRGSDLFSPKDAVIAITKQFLKGKGKVENVYTQHQPLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLDRRPQDIIIVFVIIGGATYEALTVYNLNRTTPGVRIVLGGTIVHNT	540
	:		
Db	481	KLKESLYPYLGPSTLDRRPQDIIIVFVIIGGATYEALTVYNLNRTTPGVRIVLGGTIVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSAASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSAASRR	570

RESULT 6

VPS45_MOUSE

ID VPS45_MOUSE Reviewed; 570 AA.
 AC P97390; Q91VK9;
 DT 19-SEP-2002, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1997, sequence version 1.
 DT 05-OCT-2010, entry version 76.
 DE RecName: Full=Vacuolar protein sorting-associated protein 45;
 DE Short=mVps45;
 GN Name=Vps45; Synonyms=Vps45a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA], AND INTERACTION WITH STX6.
 RC STRAIN=Swiss albino; TISSUE=Adipocyte;
 RX MEDLINE=97197782; PubMed=9045632; DOI=10.1074/jbc.272.10.6187;
 RA Tellam J.T., James D.E., Stevens T.H., Piper R.C.;
 RT "Identification of a mammalian Golgi Sec13-like protein, mVps45.";
 RL J. Biol. Chem. 272:6187-6193(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
 RC STRAIN=C57BL/6; TISSUE=Brain, and Mammary tumor;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 CC -!- FUNCTION: May play a role in vesicle-mediated protein trafficking
 CC from the Golgi stack through the trans-Golgi network.
 CC -!- SUBUNIT: Interacts with ZFYVE20 (By similarity). Interacts with
 CC STX6.
 CC -!- SUBCELLULAR LOCATION: Golgi apparatus membrane; Peripheral
 CC membrane protein. Endosome membrane; Peripheral membrane protein.
 CC Note=Associated with Golgi/endosomal vesicles and the trans-Golgi
 CC network.
 CC -!- SIMILARITY: Belongs to the STXBP/unc-18/SEC1 family.
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 CC -----
 DR EMBL; U66865; AAB37577.1; -; mRNA.
 DR EMBL; BC012691; AAH12691.1; -; mRNA.
 DR EMBL; BC058528; AAH58528.1; -; mRNA.
 DR IPI; IPI00124291; -.
 DR RefSeq; NP_038869.1; -.

DR UniGene; Mm.263185; -.
 DR ProteinModelPortal; P97390; -.
 DR SMR; P97390; 6-548.
 DR STRING; P97390; -.
 DR PhosphoSite; P97390; -.
 DR PRIDE; P97390; -.
 DR Ensembl; ENSMUST00000015891; ENSMUSP00000015891; ENSMUSG00000015747.
 DR GeneID; 22365; -.
 DR KEGG; mmu:22365; -.
 DR UCSC; uc008qly.1; mouse.
 DR CTID; 22365; -.
 DR MGI; MGI:891965; Vps45.
 DR eggNOG; roNOG05944; -.
 DR HOMOGENOM; HBG559243; -.
 DR HOVERGEN; HBG059810; -.
 DR InParanoid; P97390; -.
 DR OMA; GTIIHNT; -.
 DR OrthoDB; EOG9PCDBM; -.
 DR PhylomedDB; P97390; -.
 DR NextBio; 302685; -.
 DR ArrayExpress; P97390; -.
 DR Bgee; P97390; -.
 DR CleanEx; MM_VPS45; -.
 DR Genvestigator; P97390; -.
 DR GermOnline; ENSMUSG00000015747; Mus musculus.
 DR GO; GO:0010008; C:endosome membrane; IDA:MGI.
 DR GO; GO:0000139; C:Golgi membrane; IDA:MGI.
 DR GO; GO:0005515; F:protein binding; IPI:MGI.
 DR GO; GO:0015031; P:vesicle docking involved in exocytosis; IEA:UniProtKB-KW.
 DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.
 DR InterPro; IPR001619; Sec1-like.
 DR PANTHER; PTHR11679; Sec1-like; 1.
 DR Pfam; PF00995; Sec1; 1.
 DR SUPFAM; SSF56815; Sec1-like; 1.
 PE 1: Evidence at protein level;
 KW Endosome; Golgi apparatus; Membrane; Protein transport; Transport.
 FT CHAIN 1 570 Vacuolar protein sorting-associated
 FT protein 45.
 FT /FTId=PRO_0000206313.
 FT CONFLICT 55 55 I -> M (in Ref. 2; AAH12691).
 SQ SEQUENCE 570 AA; 65053 MW; DA704FDE8469F488 CRC64;

Query Match 98.1%; Score 2844; DB 1; Length 570;
 Best Local Similarity 97.0%;
 Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGTIVSMVTQSEILQKEVYLFERIDSQRN 60
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGTIVSMVTQSEILQKEVYLFERIDSQRN 60

 Qy 61 EIMKHLKAICFLRPTKENVDIYIQLERPRKYTIYIFIYFSNVISKSVDVKS LAEADEQE VVA 120
 ||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 EIMKHLKAICFLRPTKENVEYL IQLELRPKYSIYIFIYFSNVISKSVDVKS LAEADEQE VVA 120

 Qy 121 EVQEYFGDYIAVNPHLFSLNILGCCQGRNWPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
 |||||||:|||||:|||||:
 Db 121 EVQEYFGDYIAVNPHLFSLNILGCCQGRNWPAQLSRTTQGLTALLSLKKCPMIRYQLS 180

 Qy 181 SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
 ||||:|||||:|||||:
 Db 181 SEAAKRLGECKVQKVISKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

 Qy 241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNL MEDFQKKPK 300
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 Db 241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNL MEDFQKKPK 300

 Qy 301 EQQKLESIADMKA FVENY PQFKKMSGTVS KHVTVV GELS RL VSERNL LEVSE VEQELACQ 360
 |||||||:
 Db 301 EQQKLESIADMKA FVENY PQFKKMSGTVS KHVTVV GELS RL VSERNL LEVSE VEQELACQ 360

Qy	361	NDHSSLALQNIKRLLQNPKVTEFDAARLVLMLYALHYERHSSNSLPGLMMMDLRNKGVSSEKYR	420
Db	361	NDHSSLALQNVKRRLQNPKVTEFDAARLVLMLYALHYERHSSNSLPGLIVDLSRSKGVAEKYR	420
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKDAVITA	480
	K	QFLKLGLKG	
Db	421	KLVSAVVEYGGKRVRGSDLFSPKDAVITA	480
Qy	481	RLKENLYPYLGSTLDRPQDIIVFVIGGATYEEALTVYLNRTTPGVRLVGGTTVHNT	540
Db	481	RLKENLYPYLGSTLDRPQDIIVFVIGGATYEEALTVYLNRTTPGVRLVGGTTVHNT	540
Qy	541	KSFLEEVLASGLHRSRSKESSQVTSRSA	570
Db	541	KSFLEEVLASGLHRSRSKESSQVTSRSA	570

RESULT 7

Q3THX4_MOUSE

ID Q3THX4_MOUSE Unreviewed; 570 AA.
AC Q3THX4;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 05-OCT-2010, entry version 31.
DE SubName: Full=Putative uncharacterized protein;
GN Name=Vps45;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=DBA/2;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aiden V., Allen J.E.,
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dallymale E., Dalrymple B.P., de Boni B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakob M., Kanapin A., Katch M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Koliatis G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareaux L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasakai D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Immura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Koijima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,

RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563 (2005).
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 CC -----
 DR EMBL; AK146190; BAE26966.1; -; mRNA.
 DR EMBL; AK168101; BAE40072.1; -; mRNA.
 DR IPI; IPI00124291; -.
 DR UniGene; Mm.263185; -.
 DR ProteinModelPortal; Q3THX4; -.
 DR STRING; Q3THX4; -.
 DR Ensembl; ENSMUST0000015891; ENSMUSP0000015891; ENSMUSG0000015747.
 DR MGI; MGI:891965; Vps45.
 DR HOVERGEN; HBG059810; -.
 DR InParanoid; Q3THX4; -.
 DR ArrayExpress; Q3THX4; -.
 DR BeeGee; Q3THX4; -.
 DR Genevestigator; Q3THX4; -.
 DR GO; GO:0010008; C:endosome membrane; IDA:MGI.
 DR GO; GO:0000139; C:Golgi membrane; IDA:MGI.
 DR GO; GO:0005515; F:protein binding; IPI:MGI.
 DR GO; GO:0006904; Pivesicle docking involved in exocytosis; IEA:InterPro.
 DR InterPro; IPR001619; Sec1-like.
 DR PANTHER; PTHR11679; Sec1-like; 1.
 DR Pfam; PF00995; Sec1; 1.
 DR SUPFAM; SSE56815; Sec1-like; 1.
 PE 2: Evidence at transcript level;
 SQ SEQUENCE 570 AA; 65039 MW; DA6CBDD7967C1488 CRC64;

Query Match 98.0%; Score 2841; DB 2; Length 570;
 Best Local Similarity 96.8%;
 Matches 552; Conservative 15; Mismatches 3; Indels 0; Gaps 0;

 Qy 1 MNVVFAVKYQYISKMIEDSGPGMKVLLMDKETTGTIVSVMVTQSEILQKEVYLFERIDSQRN 60
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 Db 1 MNVVFAVKYQYISKMIEDSGPGMKVLLMDKETTGTIVSVMVTQSEILQKEVYLFERIDSQRN 60

 Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIIFYFSNVISKSDVKS LAEADEQEVVAA 120
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 EIMKHLKAICFLRPTKENVEYLQIELRRPKYSIIFYFSNVISKSDVKS LAEADEQEVVAA 120

 Qy 121 EVQEYFGDYIAVNPHLFSLNLIGCCQGRNWDPAQLSRTTQGLTALLLSLKCPMIRYQLS 180
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 121 EVQEYFGDYIAVNPHLFSLNLIGCCQGRNWDPAQLSRTTQGLTALLLSLKCPMIRYQLS 180

 Qy 181 SEAARKRLACVKQVITKEYELEFRRTEVPPLLLIDRCDDA1TPLLNQWTYQAMVHELL 240
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 181 SEAARKRLGECEVRQVISKEYELEFRRTEVPPLLLIDRCDDA1TPLLNQWTYQAMVHELL 240

 Qy 241 GINNNRIDLDSRVPGISKDLREVVLSAENDEFYANNMLNFAEIGSNIKNLMEDFQKKPK 300
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 241 GINNNRIDLDSRVPGISKDLREVVLSAENDEFYANNMLNFAEIGSNIKNLMEDFQKKRPK 300

 Qy 301 EQQKLESIADMKADEVNYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
 |||||||:|||||:|||||:|||||:|||||:|||||:
 Db 301 EQQKLESIADMKADEVNYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360

 Qy 361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVEKYR 420
 |||||||:|||||:|||||:|||||:|||||:
 Db 361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR 420

 Qy 421 KLVSADVVEYGGKRVRGSDLFSPKDAVITAQKFLKGKGVENVYTQHQPFHLHETLDHLIKG 480
 |||||||:|||||:|||||:|||||:
 Db 421 KLVSADVVEYGGKRVRGSDVFSPKDAVITAQKFLKGKGVENVYTQHQPFHLHETLDHLIKG 480

 Qy 481 RLKENLYPILGPSTLDRDPRQDIIIFVIGGATYEALTVYNLNRTTPGVRIVLGTTVHN 540
 |||||||:|||||:|||||:

Db 481 RLKENLYPVLGPSTLDRRPQDIIIVFIIGGATYEEALTVYNLNRTTPGVRIVLGTTIHNT 540

Qy 541 KSFLEEVLASGLHSRSKESSQVTSRASR 570
|||||:|||||:|||||:|||:|||

Db 541 KSFLEEVLASGLHSRSRESSQATSRSANRR 570

RESULT 8

VPS45_RAT

ID VPS45_RAT Reviewed; 570 AA.

AC O08700;

DT 19-SEP-2002, integrated into UniProtKB/Swiss-Prot.

DT 01-JUL-1997, sequence version 1.

DT 05-OCT-2010, entry version 67.

DE RecName: Full=Vacuolar protein sorting-associated protein 45;

DE Short=rVps45;

GN Name=Vps45; Synonyms=Vps45a;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA].

RC TISSUE=Brain;

RX MEDLINE=97260358; PubMed=9106478; DOI=10.1016/S0005-2736(97)00014-X;

RA El-Husseini A.E.-D.; Guthrie H.; Snutch T.P.; Vincent S.R.;

RT "Molecular cloning of a mammalian homologue of the yeast vesicular transport protein vps45.";

RL Biochim. Biophys. Acta 1325:8-12(1997).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Heart;

RX PubMed=15489334; DOI=10.1101/gr.2596504;

RG The MGC Project Team;

RT "The status, quality, and expansion of the NIH full-length cDNA

RT project: the Mammalian Gene Collection (MGC).";

RL Genome Res. 14:2121-2127(2004).

CC -!- FUNCTION: May play a role in vesicle-mediated protein trafficking
CC from the Golgi stack through the trans-Golgi network.

CC -!- SUBUNIT: Interacts with STX6 and ZFYVE20 (By similarity).

CC -!- SUBCELLULAR LOCATION: Golgi apparatus membrane; Peripheral
CC membrane protein (By similarity). Endosome membrane; Peripheral
CC membrane protein (By similarity). Note=Associated with
CC Golgi/endosomal vesicles and the trans-Golgi network (By
CC similarity).CC -!- TISSUE SPECIFICITY: Ubiquitous; expression was highest in testis
CC and in brain. Detected in every part of the brain.

CC -!- SIMILARITY: Belongs to the STXBP/unc-18/SEC1 family.

CC -----

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CC -----

DR EMBL; U81160; AAB53041.1; -; mRNA.

DR EMBL; BC081705; AAH81705.1; -; mRNA.

DR IPI; IPI00195452; -.

DR RefSeq; NP_742069.1; -.

DR UniGene; Rn.9316; -.

DR ProteinModelPortal; O08700; -.

DR SMR; O08700; 6-548.

DR MINT; MINT-4576687; -.

DR STRING; O08700; -.

DR PRIDE; O08700; -.

DR Ensembl; ENSRNOT00000028751; ENSRNP00000028751; ENSRNOG00000021173.

DR GeneID; 64516; -.

DR KEGG; rno:64516; -.

DR UCSC; NM_172072; rat.

DR CTD; 64516; -.

DR RGD; 621267; Vps45.

DR eggNOG; roNOGO5944; -.

HOVERGEN; HBG059810; -.
 DR InParanoid; O08700; -.
 DR OMA; GTTIHNHT; -.
 DR OrthoDB; EOG9FCDBM; -.
 DR PhylomeDB; O08700; -.
 DR NextBio; 613314; -.
 DR ArrayExpress; O08700; -.
 DR Genevestigator; O08700; -.
 DR GermOnline; ENSRNOG00000021173; Rattus norvegicus.
 DR GO; GO:0010008; C:endosome membrane; IEA:UniProtKB-SubCell.
 DR GO; GO:0001393; C:Golgi membrane; IEA:UniProtKB-SubCell.
 DR GO; GO:0015031; P:protein transport; IEA:UniProtKB-KW.
 DR GO; GO:0006904; P:fusicle docking involved in exocytosis; IEA:InterPro.
 DR InterPro; IPR001619; Sec1-like.
 DR PANTHER; PTHR11679; Sec1-like; 1.
 DR Pfam; PF00995; Sec1; 1.
 DR SUPFAM; SSF56815; Sec1-like; 1.
 PE 2: Evidence at transcript level;
 KW Endosome; Golgi apparatus; Membrane; Protein transport; Transport.
 FT CHAIN 1 570 Vacuolar protein sorting-associated
 FT protein 45.
 FT /FTId=PRO_0000206314.
 SQ SEQUENCE 570 AA; 64894 MW; OFF5E2D8E7E7E571 CRC64;

Query Match 98.0%; Score 2840; DB 1; Length 570;
 Best Local Similarity 97.2%;
 Matches 554; Conservative 12; Mismatches 4; Indels 0; Gaps 0

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Qy      1 MNVVFAVKQYIISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEIIQLKEVYLFERIDSQRN 6
Db      1 MNVVFAVKQYIISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEIIQLKEVYLFERIDSQRN 6

Qy      61 EIMKHLKAICFLRPDKENVDYIIQELRRPKTYIIFYIFSNVISKSVDVSKLAEADEQEYVVA 1
Db      61 EIMKHLKAICFLRPDKENVDLSIQLQELRRPKYSIYIFYIFSNVISKSVDVSKLAEADEQEYVVA 1

Qy      121 EVQEYFGDYIAVNPHLFLSNIILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 1
Db      121 EVQEYFGDYIAVNPHLFLSNIILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 1

Qy      181 SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 2
Db      181 SEAAKRLGECVKQVISKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 2

Qy      241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNAEIGNSNIKNLMEDFQKKPK 3
Db      241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNAEIGNSNIKNLMEDFQKKPK 3

Qy      301 EQQKLESIADMKADEVNPQFKKMSGTVSKHVTVGELSRLVSENRNLLEVSEVEQELACQ 3
Db      301 EQQKLESIADMKADEVNPQFKKMSGTVSKHVTVGELSRLVSENRNLLEVSEVEQELACQ 3

Qy      361 NDHSSALQNQKRLQQNPKVTEFDAARLVLMLYALHYERHSSNLPGLMMMDLRNKGVSEKYR 4
Db      361 NDHSSALQNQVKRLLQNPKVTEFDAVRLVMLYALHYERHSSNLPGLIVDLRSKGVAEYKR 4

Qy      421 KLVSAVVEYGGKRVRGSDFLSPKDADAVITAQKFILGKLGKGVENVYQTQHQFFLHETLDHLIKG 4
Db      421 KLVSAVVEYGGKRVRGSDFLSPKDADAVITAQKFILGKLGKGVENVYQTQHQFFLHETLDHLIKG 4

Qy      481 RLKENLYPYLGPSTLDRDPQDIIVFVIGGATYYEALTVYNLNRTTPGVRIVLGGTTVINT 5
Db      481 RLKENLYPYLGPSTLDRDPQDIIVFVIGGATYYEALTVYNLNRTTPGVRIVLGGTTVINT 5

Qy      541 KSFLEEVLASGLHGRSKESQSVTSRSASRR 570
Db      541 KSFLEEVLASGLHGRSRSESQGATRSASRR 570
  
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RESULT

B72360_HUMAN
ID B72360_HUMAN Unreviewed; 534 AA.
AC B72360;
DT 03-MAR-2009, integrated into UniProtKB/TrEMBL.
DT 03-MAR-2009, sequence version 1.
DT 05-OCT-2010, entry version 11.
DE SubName: Full= cDNA FLJ54353, highly similar to Vacuolar protein sorting-associated protein 45;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hippocampus;
RA Wakamatsu A., Yamamoto J., Kimura K., Ishii S., Watanabe K.,
RA Sugiyama A., Murakawa K., Kaida T., Tsuchiya K., Fukuzumi Y.,
RA Kumagai A., Oishi Y., Yamamoto S., Ono Y., Komori Y., Yamazaki M.,
RA Kis Y., Nishikawa T., Sugano S., Nomura N., Isogai T.;
RT "NEDO human cDNA sequencing project focused on splicing variants.";
RL Submitted (OCT-2007) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AK295529; BAH12096.1; -; mRNA.
DR IPI; IPI00090327; -.
DR UniGene; Hs.443750; -.
DR Ensembl; ENST00000369130; ENSP0000358126; ENSG00000136631.
DR HGNC; HGNC:14579; VPS45.
DR HOVERGEN; HBG059810; -.
DR Bgee; B72360; -.
DR GO; GO:0006904; Pivesicle docking involved in exocytosis; IEA:InterPro.
DR InterPro; IPR001619; Sec1-like.
DR PANTHER; PTHR11679; Sec1-like; 1.
DR Pfam; PF00995; Sec1; 1.
DR SUPFAM; SSF56815; Sec1-like; 1.
PE 2: Evidence at transcript level;
SQ SEQUENCE 534 AA; 61107 MW; 8FC6896E27D62D59 CRC64;

Query Match 93.7%; Score 2716; DB 2; Length 534;
Best Local Similarity 99.8%;
Matches 533; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 37 MVYTQEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKTYIFI 96
Db |||||||
Qy 97 YFSNVISKSDVKSLAEADEQEVVAEVQEFYGDYIAVNPFLSFLNIIGCCQGRNWDPQAQLS 156
Db 61 YFSNVISKSDVKSLAEADEQEVVAEVQEFYGDYIAVNPFLSFLNIIGCCQGRNWDPQAQLS 120
Qy 157 RTTQGLTALLSLKKCPMIRYQLSSEAAKRLAECVQKVITKEYELFEFRRTTEVPPLLLL 216
Db |||||||
Qy 217 DRCDDAITPLLNQNTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDFYANMM 276
Db |||||||
Qy 277 YLNFABIGSNIKNLMEDFQKKPKEQQQKLESIADMKAFFENYQPQFKKMSGTVSKHVTVG 336
Db 241 YLNFABIGSNIKNLMEDFQKKPKEQQQKLESIADMKAFFESYPQFKKMSGTVSKHVTVG 300
Qy 337 ELSRLVSENRNLLEVSEVEQELACQNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYE 396
Db |||||||
Qy 301 ELSRLVSENRNLLEVSEVEQELACQNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYE 360
Qy 397 RHSSNLPGLMMDLNRKGKVSEKYRKLVLSAVVEYGGKVRGSDLFSPKDAVIAITKQFLKG 456
Db |||||||

SCORE Search Results Details for Application 09556178

[Score Home](#) [Page Retrieve](#) [Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 09556178 and Search Result 20101203_114247_us-09-556-178-1_rpr

GenCore version 6.3
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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:52 ; Search time 10 Seconds
(without alignments)
5484.359 Million cell updates/sec

Title: US-09-556-178-1
Perfect score!: 2898
Sequence: 1 MNVVFAVWQYIISKMEIDSGP.....GLNRSRSNESSQVTSRASRR 570

Scoring table: BL0SUM62
Gappen 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 49 summaries

Database : PIR_BO1:
1: pir1*
2: pir2*
3: pir3*
4: pir4*
SUMMARIES

Result	Query	No.	Score	Match Length	DB	ID	Description
		1	2898	9.7	JCS722		vacuolar protein s
		2	1289	44.8	569	T22056	vacuolar protein s
		3	1296	44.7	569	2 TO0445	vacuolar protein-s
		4	1267.5	41.7	547	2 T29567	hypothetical prote
		5	1137.5	39.3	558	2 S62458	vacuolar protein s
		6	1137.5	39.3	573	2 S62458	VPS34-like protein ye
		7	778.5	26.9	722	2 D71407	VPS34-like protein
		8	386.5	13.3	593	2 A59531	nu Seel protein -
		9	382	13.2	648	2 JC4674	Slyl protein - rat
		10	376.5	13.0	594	2 A57022	Munc18-2 - rat
		11	376.5	13.0	595	2 A57022	hypothetical prote
		12	366	12.6	639	2 T41585	stxbp-unc-18-secl
		13	361	12.5	673	2 S36747	probable acetylcho
		14	356	12.2	592	2 I49239	vesicle transport
		15	349.5	12.2	460	2 A50110	Slyl protein - yea
		16	348.5	11.9	597	2 C33378	reg protein - fruit
		17	339	11.7	733	2 C96258	protein F5C01.8 (i
		18	338.5	11.7	693	2 T14143	synaptosomal-binding p
		19	333.5	11.5	594	2 S39345	unc-18 protein hom
		20	333.5	11.5	595	2 S39345	synaptosomal-binding p
		21	331.5	11.4	707	2 T22127	hypothetical prote
		22	325.5	11.2	592	2 S39346	unc-18 protein hom
		23	315.5	10.9	562	2 T25281	hypothetical prote
		24	297	10.2	627	2 GB4558	probable SMC1 fami
		25	238	9.7	721	2 T2779	S62C1 - yeast
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		28	168	5.8	576	2 S27790	SLP1 protein homol
		29	167	5.6	693	2 A57022	vacuolar protein-s
		30	167	5.6	593	2 T27794	vacuolar protein-s
		31	159.5	5.5	617	2 JC5721	vacuolar protein s
		32	142	4.9	1008	2 A64465	hypothetical prote
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		34	138	4.7	1202	2 T27795	hypothetical prote
		35	138.5	4.6	1188	2 T4367	pyruvate water di
		36	133	4.6	944	1 S48821	probable membrane
		37	132.5	4.6	1169	2 A64505	P119 homolog - Met
		38	132.5	4.6	3229	2 IS2100	giantin - human
		39	132.5	4.6	3230	2 IS2100	giantin - human
		40	132	4.6	554	2 E90401	hypothetical prote
		41	132	4.6	864	2 B90395	purine NTPase [imp
		42	132	4.6	1330	2 H89567	protein T0B9.1 (i
		43	132	4.6	1679	2 S48185	hypothetical prote
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ALIGNMENTS

RESULT 1
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vacuolar protein sorting protein 45 - human
C:Species: Homo sapiens [man]
C:Date: 09-Dec-1997 #sequence revision 09-Dec-1997 #text_change 09-Jul-2004
C:Accession: JC5722
R:Fewerstor, J.; Haas, S.C.; Hyde, F.S.; Scheller, R.H.
GenBank; 183; 1994
A:Title: Mammalian homologues of yeast vacuolar protein sorting (vps) genes implicated in Golgi-to-lysosome trafficking.
A:Reference number: JC5720; MUID: 97149272; PMID: B8996080
A:Accession: JC5722
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

SCORE Search Results Details for Application 09556178
and Search Result 20101203_114248_us-09-556-178-
1.raj.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 09556178 and Search Result 20101203_114248_us-09-556-178-1.ra1.

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GenCore version 6.3
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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:52 ; Search time 57 Seconds
(without alignments)
3961.810 Million cell updates/sec

Title: US-09-556-178-1
Perfect score: 2898
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2170800 seqs, 396181022 residues

Total number of hits satisfying chosen parameters.: 2170800

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /ABSS/Data/CRF/ptodata/1/iaa/H_COMB.pep:*
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6: /ABSS/Data/CRF/ptodata/1/iaa/RE_COMB.pep:*
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                                SUMMARIES
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1	2898	100.0	570	1	US-08-967-364-1	Sequence 1, Appli	
2	2898	100.0	570	2	US-09-368-408-1	Sequence 1, Appli	
3	2898	100.0	570	3	US-10-511-937-2612	Sequence 2612, Ap	
4	2898	100.0	570	3	US-11-443-428A-738990	Sequence 738990,	
5	2898	100.0	570	3	US-11-443-428A-738993	Sequence 738993,	
6	2898	100.0	570	3	US-11-443-428A-738994	Sequence 738994,	
7	2898	100.0	570	3	US-11-443-428A-739003	Sequence 739003,	
8	2844	98.1	570	1	US-08-967-364-7	Sequence 7, Appli	
9	2844	98.1	570	2	US-09-368-408-7	Sequence 7, Appli	
10	2783	96.0	552	3	US-11-443-428A-738991	Sequence 738991,	

11	2777	95.8	552	3	US-11-443-428A-738998	Sequence 738998,
12	2769	95.5	612	3	US-11-443-428A-739002	Sequence 739002,
13	2721	93.9	534	3	US-11-443-428A-738992	Sequence 738992,
14	2721	93.9	534	3	US-11-443-428A-739001	Sequence 739001,
15	2550	88.0	526	3	US-11-443-428A-739004	Sequence 739004,
16	1873	64.6	372	3	US-11-443-428A-738999	Sequence 738999,
17	1755	60.6	359	3	US-11-443-428A-738995	Sequence 738995,
18	1273	43.9	567	3	US-11-241-607-62939	Sequence 62939, A
19	976	33.7	577	2	US-09-487-558B-420	Sequence 420, App
20	917	31.6	398	3	US-10-703-032-125739	Sequence 125739,
21	788	27.2	162	3	US-11-443-428A-739006	Sequence 739006,
22	786.5	27.1	329	3	US-09-417-507-33074	Sequence 33074, A
23	757.5	26.1	200	3	US-11-443-428A-738996	Sequence 738996,
24	744	25.7	158	3	US-11-443-428A-739005	Sequence 739005,
25	613	21.2	129	3	US-11-443-428A-739000	Sequence 739000,
26	492	17.0	230	3	US-10-767-701-43244	Sequence 43244, A
27	416	14.4	212	3	US-09-417-507-33075	Sequence 33075, A
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34	382.5	13.2	593	1	US-08-900-927-1	Sequence 1, Appli
35	382.5	13.2	593	1	US-09-191-279-1	Sequence 1, Appli
36	382.5	13.2	593	2	US-09-334-476-1	Sequence 1, Appli
37	382.5	13.2	593	3	US-11-483-373B-2	Sequence 2, Appli
38	382.5	13.2	609	3	US-11-443-428A-857469	Sequence 857469,
39	380.5	13.1	632	3	US-11-443-428A-893751	Sequence 893751,
40	380	13.1	617	3	US-11-443-428A-893748	Sequence 893748,
41	380	13.1	648	3	US-11-443-428A-893749	Sequence 893749,
42	380	13.1	651	3	US-11-443-428A-893754	Sequence 893754,
43	380	13.1	651	3	US-11-443-428A-893758	Sequence 893758,
44	378	13.0	644	3	US-11-443-428A-857458	Sequence 857458,
45	372	12.8	619	3	US-11-443-428A-857474	Sequence 857474,

ALIGNMENTS

RESULT 1
 US-08-967-364-1
; Sequence 1, Application US/08967364
; Patent No. 5989859
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,364
; FILING DATE: No. 5989859ember 7, 1997

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; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPIPEB01
; CLONE: 75871
US-08-967-364-1

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Query Match 100.0%; Score 2898; DB 1; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	121 EVQEFGYDGYIAVNPHLFLSNIILGCCQGRNWDPQAQLSRITQGLTALLLSKKCPMIRYQLS 180
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RESULT 2

US-09-368-408-1
; Sequence 1, Application US/09368408
; Patent No. 6071703
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/368,408
; FILING DATE:
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/967,364
; FILING DATE:
ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPIPEB01
; CLONE: 75871

US-09-368-408-1

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Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 2612, Application US/10511937
; Patent No. 7691569
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2612
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2612

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Db	121 EVQEFGYGDYIAVNPHLFSNLILGCCQGRNWDPAQQLSRTTQGLTALLLSLKCPMIRYQLS 180
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Db	181 SEA A K R L A E C V K Q V I T K E Y E L F E F R R T E V P P L L L I L D R C D D A I T P L L N Q W T Y Q A M V H E L L 240
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Db	241 G I N N N R I D L S R V P G I S K D L R E V V L S A E N D E F Y A N N M Y L N F A E I G S N I K N L M E D F Q K K P K 300
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RESULT 4

US-11-443-428A-738990
; Sequence 738990, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738990
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738990

Query Match 100.0%; Score 2898; DB 3; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
Qy	61 EIMKHLKAICFLRPTKENVDYIIQELRPRKYTIYIFIYFSNVISKSDVKS LAEADEQE VVA 120
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Db	121 EVQEFGDYIAVNPHLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
Qy	181 SEA AKRLAE CVKQVITKEYELF EFR RTEV PPLL LIDRC DDA ITPL LNQWTY QAMV HELL 240
Db	181 SEA AKRLAE CVKQVITKEYELF EFR RTEV PPLL LIDRC DDA ITPL LNQWTY QAMV HELL 240
Qy	241 GINNNRIDLSRVPGISKD LRE VLSA E NDEF YAN NM YLN FAEIG SNI KNL MEDF QKKPK 300
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Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMMDLRNKGVSEK YR 420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMMDLRNKGVSEK YR 420
Qy	421 KL VSAV VEYGGK RVGSDL FSPK DAVA ITKQFLK GLKG VEN VY TQHQ PFLH ETLDH LIKG 480
Db	421 KL VSAV VEYGGK RVGSDL FSPK DAVA ITKQFLK GLKG VEN VY TQHQ PFLH ETLDH LIKG 480
Qy	481 RL KENLYP YLG PSTL RDRP QDII V FV IGGAT YEE ALTV YN LN RTT PGV RIV LG GTT VHNT 540
Db	481 RL KENLYP YLG PSTL RDRP QDII V FV IGGAT YEE ALTV YN LN RTT PGV RIV LG GTT VHNT 540
Qy	541 KSFLEEV LASGLHSRSK ESSQ VTSR SASR 570
Db	541 KSFLEEV LASGLHSRSK ESSQ VTSR SASR 570

RESULT 5

US-11-443-428A-738993

; Sequence 738993, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738993

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738993

Query Match 100.0%; Score 2898; DB 3; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
 |||||||
 Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60

Qy 61 EIMKHLKAICFLRPTKENVYDIIQELRPRKYTIYIFIYFSNVISKSDVKS LAEADEQE VVA 120
 |||||||
 Db 61 EIMKHLKAICFLRPTKENVYDIIQELRPRKYTIYIFIYFSNVISKSDVKS LAEADEQE VVA 120

Qy 121 EVQEFGYD YIAVNPHLFSLNILGCCQGRNWDP AQLSRTT QGLTALLSLKKC P MIR YQLS 180
 |||||||
 Db 121 EVQEFGYD YIAVNPHLFSLNILGCCQGRNWDP AQLSRTT QGLTALLSLKKC P MIR YQLS 180

Qy 181 SEA AKRLAECV KVQVITKEYELF EFR RTEV PPLL LIDRC DDA ITPL LNQWTY QAMV HELL 240
 |||||||
 Db 181 SEA AKRLAECV KVQVITKEYELF EFR RTEV PPLL LIDRC DDA ITPL LNQWTY QAMV HELL 240

Qy 241 GINNNRIDLSRVPGIS KDLRE VVLSAENDEF YAN NMYLNF AIG SNIKNL MEDF QKKPK 300
 |||||||
 Db 241 GINNNRIDLSRVPGIS KDLRE VVLSAENDEF YAN NMYLNF AIG SNIKNL MEDF QKKPK 300

Qy 301 EQQKLESIADMKA FVENY PQFKKMSGT VSKH VT VVGEL SRLV SERNL LEV SEVE QELACQ 360
 |||||||
 Db 301 EQQKLESIADMKA FVENY PQFKKMSGT VSKH VT VVGEL SRLV SERNL LEV SEVE QELACQ 360

Qy 361 NDHSSALQNIK RLLQNPKVTEFDAARLVM LYALHYERHSSNSLPGLMM DLRNKGVSEK YR 420
 |||||||
 Db 361 NDHSSALQNIK RLLQNPKVTEFDAARLVM LYALHYERHSSNSLPGLMM DLRNKGVSEK YR 420

Qy 421 KL VSAVVEYGGK RVRGSDL FSPK DAVA ITKQFLKG LKG VEN VYTQHQ PFLH ETLDH LIKG 480
 |||||||
 Db 421 KL VSAVVEYGGK RVRGSDL FSPK DAVA ITKQFLKG LKG VEN VYTQHQ PFLH ETLDH LIKG 480

Qy 481 RLKENLYP YLGP STLRDRP QD IIIVF VIGGAT YEEALT VY NLN RTT PGVR IVLG GTTV HNT 540
 |||||||
 Db 481 RLKENLYP YLGP STLRDRP QD IIIVF VIGGAT YEEALT VY NLN RTT PGVR IVLG GTTV HNT 540

Qy 541 KSFLEEVLASGLHSRSKES SQVTSRSASRR 570
 |||||||
 Db 541 KSFLEEVLASGLHSRSKES SQVTSRSASRR 570

RESULT 6

US-11-443-428A-738994
 ; Sequence 738994, Application US/11443428A
 ; Patent No. 7745391
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hanqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443,428A
 ; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738994
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738994

Query Match 100.0%; Score 2898; DB 3; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60

Qy 61 EIMKHLKAICFLRPTKENVDDIIQELRPRKYTIYIYFSNVISKSDVKS LAEADEQEVV A 120
Db 61 EIMKHLKAICFLRPTKENVDDIIQELRPRKYTIYIYFSNVISKSDVKS LAEADEQEVV A 120

Qy 121 EVQEFYGDYIAVNPHLFLSNI LGCCQGRNWDPQLSRTTQGLTALLLSLKCPMIRYQLS 180
Db 121 EVQEFYGDYIAVNPHLFLSNI LGCCQGRNWDPQLSRTTQGLTALLLSLKCPMIRYQLS 180

Qy 181 SEAAKRLAECKVQVITKEYELFEFRRTEVPPLLILDRCDDAITPLLNQWTYQAMVHELL 240
Db 181 SEAAKRLAECKVQVITKEYELFEFRRTEVPPLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy 241 GINNNRIDLSRVPGISKDREV VLSAENDEFYANNMYLNF AEIGSNIKNL MEDFQKKPK 300
Db 241 GINNNRIDLSRVPGISKDREV VLSAENDEFYANNMYLNF AEIGSNIKNL MEDFQKKPK 300

Qy 301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVT VVGEL SRLVSE RNLLLEV SEVE QELACQ 360
Db 301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVT VVGEL SRLVSE RNLLLEV SEVE QELACQ 360

Qy 361 NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKGVSEK YR 420
Db 361 NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKGVSEK YR 420

Qy 421 KLVSAAVVEYGGKRVRGSDLFSPKDAV AITKQFLKG LKG VEN VYTQHQPF LHETLDH LING 480
Db 421 KLVSAAVVEYGGKRVRGSDLFSPKDAV AITKQFLKG LKG VEN VYTQHQPF LHETLDH LING 480

Qy 481 RLKENLYPYLGPSTL RDRPQD IIVFVI GGATYE EALT VYVNLNR TPPGVRIVLGTTVHN T 540
Db 481 RLKENLYPYLGPSTL RDRPQD IIVFVI GGATYE EALT VYVNLNR TPPGVRIVLGTTVHN T 540

Qy 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
Db 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

RESULT 7

US-11-443-428A-739003
; Sequence 739003, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen

;
 APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443,428A
 ; CURRENT FILING DATE: 2006-05-31
 ; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 739003
 ; LENGTH: 570
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-443-428A-739003

Query Match 100.0%; Score 2898; DB 3; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
Qy	61 EIMKHLKAICFLRPTKENVDYIIQELRPKTYIYIFIYFSNVISKSDVKSLSAEADEQEVVVA 120
Db	61 EIMKHLKAICFLRPTKENVDYIIQELRPKTYIYIFIYFSNVISKSDVKSLSAEADEQEVVVA 120
Qy	121 EVQEFGYGDYIAVNPHLFLSNIILGCCQGRNWDPAPQLSRTTQGLTALLLSKKCPMIRYQLS 180
Db	121 EVQEFGYGDYIAVNPHLFLSNIILGCCQGRNWDPAPQLSRTTQGLTALLLSKKCPMIRYQLS 180
Qy	181 SEAARKLAECVKQVITKEYELFEFRRTVEPPLLILIDRCDDA1TPLLNQWTYQAMVHELL 240
Db	181 SEAARKLAECVKQVITKEYELFEFRRTVEPPLLILIDRCDDA1TPLLNQWTYQAMVHELL 240
Qy	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 300
Db	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 300
Qy	301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
Db	301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMMDLRNKGVSEKyr 420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMMDLRNKGVSEKyr 420
Qy	421 KLVSAVVEYGGKRVRGSDLFSPKDAAVATKQFLKGLKGVENVYTQHQPLHETLDHLIKG 480
Db	421 KLVSAVVEYGGKRVRGSDLFSPKDAAVATKQFLKGLKGVENVYTQHQPLHETLDHLIKG 480
Qy	481 RLKENLYPILGPSTLDRDPQDIIVFVIGGATYEALTVYVNLNRTPGVRIVLGTTVHNT 540
Db	481 RLKENLYPILGPSTLDRDPQDIIVFVIGGATYEALTVYVNLNRTPGVRIVLGTTVHNT 540
Qy	541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
Db	541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

RESULT 8

US-08-967-364-7
 ; Sequence 7, Application US/08967364
 ; Patent No. 5989859
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Guegler, Karl J.

; APPLICANT: Shah, Purvi
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/967,364
 ; FILING DATE: No. 5989859ember 7, 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cerrone, Michael C.
 ; REGISTRATION NUMBER: 39,132
 ; REFERENCE/DOCKET NUMBER: PF-0417 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 570 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: GI7703494
 US-08-967-364-7

Query Match 98.1%; Score 2844; DB 1; Length 570;
 Best Local Similarity 97.0%;
 Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQNR 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQNR 60
Qy	61 EIMKHLKAICFLRPTKENVDDIYIQLERRPKYTIYIFIYFSNVISKSDVKSLSAEADEQEVVVA 120
	:
Db	61 EIMKHLKAICFLRPTKENVEYLQIELRRPKSYIYIFIYFSNVISKSDVKSLSAEADEQEVVVA 120
Qy	121 EVQEFGYDGYIAVNPHFLSFLNILGCCQGRNNWDPAQLSRTTQGLTALLSSLKKCPMIRYQLS 180
Db	121 EVQEFGYDGYIAVNPHFLSFLNILGCCQGRNNWDPAQLSRTTQGLTALLSSLKKCPMIRYQLS 180
Qy	181 SEAARKLAECAVKQVITKEYELFEFRRTVEPVLILLDRCDDAITPLLNQWTYQAMVHELL 240
Db	181 SEAARKLGECAVKQVISKEYELFEFRRTVEPVLILLDRCDDAITPLLNQWTYQAMVHELL 240
Qy	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 300
	:
Db	241 GINNNRIDLSRVPGISKDLREVVLNAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKRPK 300
Qy	301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
Db	301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360

Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
	: : : : : : : : : : :
Db	361 NDHSSALQNVKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR 420
Qy	421 KLVSAAVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480
	: : : : : : : : : :
Db	421 KLVSAAVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480
Qy	481 RLKENLYPYLGPSTLRDRPQDIIVFVIIGGATYEALTVYNLNRTTPGVRIVLGTTVHNNT 540
	: : : : : : : : : :
Db	481 RLKENLYPYLGPSTLRDRPQDIIVFVIIGGATYEALTVYNLNRTTPGVRIVLGTTIHNNT 540
Qy	541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
	: : : : : :
Db	541 KSFLEEVLASGLHSRSRESSQATRSANRR 570

RESULT 9

US-09-368-408-7

; Sequence 7, Application US/09368408

; Patent No. 6071703

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/368,408
; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/967,364
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PP-0417 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 570 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: GI7703494

US-09-368-408-7

Query Match 98.1%; Score 2844; DB 2; Length 570;

Best Local Similarity 97.0%;
 Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTOSEILOKEVYLFERIDSQRN 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTOSEILOKEVYLFERIDSQRN 60
Qy	61 EIMKHLKAICFLRPTKENVDYIQLERPKTYIIFYISNVISKSDVKS LAEADEQEVV A 120
Db	61 EIMKHLKAICFLRPTKENVEYLQ ILEPKSYIIFYISNVISKSDVKS LAEADEQEVV A 120
Qy	121 EVQEFGYGDYIAVNPHFLS NLGCCGGRNWDP AQLSRTT QGLTALLLSLKCPMIRYQLS 180
Db	121 EVQEFGYGDYIAVNPHFLS NLGCCGGRNWDP AQLSRTT QGLTALLLSLKCPMIRYQLS 180
Qy	181 SEA A KRLAECV KVQVITKEYELFE FRRTEV PPLL LIDRCDDA ITPLLNQWTYQAMVHELL 240
Db	181 SEA A KRLGE C V KVQVISKEYELFE FRRTEV PPLL LIDRCDDA ITPLLNQWTYQAMVHELL 240
Qy	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNL MEDFQKKRPK 300
Db	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNL MEDFQKKRPK 300
Qy	301 EQQKLESIADMKA FVENYPQFKKMSGT SKHVTVVGELS RL VSERNLLEVSEVEQELACQ 360
Db	301 EQQKLESIADMKA FVENYPQFKKMSGT SKHVTVVGELS RL VSERNLLEVSEVEQELACQ 360
Qy	361 NDHSSALQNIK RLLQNPKVTEFDAARLVM LYALHYERHSSNSLPGLMM DLRNKG VSEK YR 420
Db	361 NDHSSALQNVK RLLQNPKVTEFDAARLVM LYALHYERHSSNSLPGLIVDLRSKGVAE KYR 420
Qy	421 KLVS AVEYGGK RVRGSDL FSPKDAV AITKQFLKG LKG VENVYTQHQ PFLHETLDH LIKG 480
Db	421 KLVS AVEYGGK RVRGSDL FSPKDAV AITKQFLKG LKG VENVYTQHQ PFLHETLDH LIKG 480
Qy	481 RLKENLYPYLGPSTLDRPQDII VFI VIGGATYEE ALTVYLN RRTTPGV RIVLG GTT VHNT 540
Db	481 RLKENLYPYLGPSTLDRPQDII VFI VIGGATYEE ALTVYLN RRTTPGV RIVLG GTT IHNT 540
Qy	541 KSFLEEVLASGLHSRSKES S QVTSRSASRR 570
Db	541 KSFLEEVLASGLHSRSQES QATSRSANRR 570

RESULT 10

US-11-443-428A-738991

; Sequence 738991, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443, 428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738991

; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738991

Query Match 96.0%; Score 2783; DB 3; Length 552;
Best Local Similarity 96.8%;
Matches 552; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 58

Qy 61 EIMKHLKAICFLRPTKENVDYI1QELRRPKTYIYIFIYFSNVISKSDVKS LAEADEQEVVVA 120
Db 59 -----ENVDYI1QELRRPKTYIYIFIYFSNVISKSDVKS LAEADEQEVVVA 102

Qy 121 EVQEFGYGDYIAVNPHLFLSNIILGCCQGRNWDPQLSRTTQGLTALLLSLKCPMIRYQLS 180
Db 103 EVQEFGYGDYIAVNPHLFLSNIILGCCQGRNWDPQLSRTTQGLTALLLSLKCPMIRYQLS 162

Qy 181 SEAARKLAECVKQVITKEYELFEFRRTEVPPLLL1LDRCDDA1TPLLNQWTYQAMVHELL 240
Db 163 SEAARKLAECVKQVITKEYELFEFRRTEVPPLLL1LDRCDDA1TPLLNQWTYQAMVHELL 222

Qy 241 GINNNRIDLSRVPGISKDRLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 300
Db 223 GINNNRIDLSRVPGISKDRLREVVL SAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 282

Qy 301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGEL SRLVSE RNLLLEVSEVEQELACQ 360
Db 283 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGEL SRLVSE RNLLLEVSEVEQELACQ 342

Qy 361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEK YR 420
Db 343 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEK YR 402

Qy 421 KLVSAVVEYGGKRVRGSDLFSPKDAV AITKQFLKGLKG VENVTQHQPF LHETLDHLIK G 480
Db 403 KLVSAVVEYGGKRVRGSDLFSPKDAV AITKQFLKGLKG VENVTQHQPF LHETLDHLIK G 462

Qy 481 RLKENLYPYLGPSTLDRPQDII1FVFIGGATYEAEALT VYVNLNRTPGVRIVLGTTVHN T 540
Db 463 RLKENLYPYLGPSTLDRPQDII1FVFIGGATYEAEALT VYVNLNRTPGVRIVLGTTVHN T 522

Qy 541 KSFLEEVLASGLHSRSKES SQVTSRSASRR 570
Db 523 KSFLEEVLASGLHSRSKES SQVTSRSASRR 552

RESULT 11

US-11-443-428A-738998
; Sequence 738998, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

;
FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738998
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738998

Query Match 95.8%; Score 2777; DB 3; Length 552;
Best Local Similarity 99.3%;
Matches 547; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
Qy	61 EIMKHLKAICFLRPTKENVDYI1QELRPRKYTIYIFIYFSNVISKSDVKSLSAEADEQEVVAA 120
Db	61 EIMKHLKAICFLRPTKENVDYI1QELRPRKYTIYIFIYFSNVISKSDVKSLSAEADEQEVVAA 120
Qy	121 EVQEFGYGDYIAVNPHFLSFLNILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180
Db	121 EVQEFGYGDYIAVNPHFLSFLNILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180
Qy	181 SEAARKLAECKVKQVITKEYELFEFRRTEVPPLLILDRCCDAITPLLNQWTYQAMVHELL 240
Db	181 SEAARKLAECKVKQVITKEYELFEFRRTEVPPLLILDRCCDAITPLLNQWTYQAMVHELL 240
Qy	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAIEGSNIKNLMEDFQKKPK 300
Db	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAIEGSNIKNLMEDFQKKPK 300
Qy	301 EQQKLESIADMKADEVNPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
Db	301 EQQKLESIADMKADEVNPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMMDLRNKGVSEKYR 420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMMDLRNKGVSEKYR 420
Qy	421 KLVSAAVVEYGGKVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFHLHETLDHLIKG 480
Db	421 KLVSAAVVEYGGKVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFHLHETLDHLIKG 480
Qy	481 RLKENLYPYLGPSTLDRPQDIIVFVIIGGATYEALTVYLNRLTPGVRIVLGTTVHN 540
Db	481 RLKENLYPYLGPSTLDRPQDIIVFVIIGGATYEALTVYLNRLTPGVRIVLGTTVHN 540
Qy	541 KS--FLEEVLA 549
Db	541 KSKRFLREGLA 551

RESULT 12

US-11-443-428A-739002
; Sequence 739002, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili

;
 APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443, 428A
 ; CURRENT FILING DATE: 2006-05-31
 ; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 739002
 ; LENGTH: 612
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-443-428A-739002

Query Match 95.5%; Score 2769; DB 3; Length 612;
 Best Local Similarity 96.5%;
 Matches 546; Conservative 5; Mismatches 11; Indels 4; Gaps 1;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
Qy	61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYIFIYFSNVISKSDVKSLSLAEADEQEVVAA 120
Db	61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYIFIYFSNVISKSDVKSLSLAEADEQEVVAA 120
Qy	121 EVQEFGYGDYIAVNPHLFSLNILGCCQGRNRWDPAPQLSRTTQGLTALLLSLKCPMIRYQLS 180
Db	121 EVQEFGYGDYIAVNPHLFSLNILGCCQGRNRWDPAPQLSRTTQGLTALLLSLKCPMIRYQLS 180
Qy	181 SEAARKLAEACVVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
Db	181 SEAARKLAEACVVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
Qy	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 300
Db	241 GINNNRIDLSRVPGISKDLREVVL SAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 300
Qy	301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLLEVSEVEQELACQ 360
Db	301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLLEVSEVEQELACQ 360
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMYLALHYERHSSNSLPGLMMMDLRNKGVSEK YR 420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMYLALHYERHSSNSLPGLMMMDLRNKGVSEK YR 420
Qy	421 KLVSAAVVEYGGKRVRGSDLFSPKD AVAITKQFLKGLKG VENVYTQHQPF LHETLDHLIKG 480
Db	421 KLVSAAVVEYGGKRVRGSDLFSPKD AVAITKQFLKGLKG VENVYTQHQPF LHETLDHLIKG 480
Qy	481 RLKENLYP LGPSTLDRPQDIIIVFVI GGATYEAEALT VYLNRLTPGV RIVLG GTTVHN T 540
Db	481 RLKENLYP LGPSTLDRPQDIIIVFVI GGATYEAEALT VYLNRLTPGV RIVLG GTTVHN T 540
Qy	541 KSFLEEVLASGLHSRSKES SQVTSRS 566
	: :: : :
Db	541 K---RAL KSHQGQR ADETVVGGRA 562

RESULT 13

US-11-443-428A-738992

; Sequence 738992, Application US/11/443428A

; Patent No. 7745391

; GENERAL INFORMATION:

;
 APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hanqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443,428A
 ; CURRENT FILING DATE: 2006-05-31
 ; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 738992
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-443-428A-738992

Query Match 93.9%; Score 2721; DB 3; Length 534;
 Best Local Similarity 100.0%;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	37 MVYTQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI	96
Db	1 MVYTQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI	60
Qy	97 YFSNVISKSDVKSLAEADEQEVVVAEVQEFYGDIYAVNPFLFSLNILGCCQGRNWDPQLS	156
Db	61 YFSNVISKSDVKSLAEADEQEVVVAEVQEFYGDIYAVNPFLFSLNILGCCQGRNWDPQLS	120
Qy	157 RTTQGLTALLLSLKKCPMIRYQLSSEAAKRLAECVKQVITKEYELFEFRTEVPPLLLIL	216
Db	121 RTTQGLTALLLSLKKCPMIRYQLSSEAAKRLAECVKQVITKEYELFEFRTEVPPLLLIL	180
Qy	217 DRCDDAITPLLNQWTYQAMVHELLGINNRRIDLRSVPGISKDLREVVLSAENDEFYANMM	276
Db	181 DRCDDAITPLLNQWTYQAMVHELLGINNRRIDLRSVPGISKDLREVVLSAENDEFYANMM	240
Qy	277 YLNFAEIGNSNIKNLMDFQKKKPKEQQKLESIADMKAFFENYPQFKKMSGTVKHVTVG	336
Db	241 YLNFAEIGNSNIKNLMDFQKKKPKEQQKLESIADMKAFFENYPQFKKMSGTVKHVTVG	300
Qy	337 ELSRLVSENRNLLEVSEVEQELACQNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYE	396
Db	301 ELSRLVSENRNLLEVSEVEQELACQNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYE	360
Qy	397 RHSSNSLPGLMMDLRNKGVSSEKYRKLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGL	456
Db	361 RHSSNSLPGLMMDLRNKGVSSEKYRKLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGL	420
Qy	457 KGVENVYTQHQPFLHETLDHLIKGRLKENLYPYLGPSTLDRDPQDIIVFVIGGATYEAL	516
Db	421 KGVENVYTQHQPFLHETLDHLIKGRLKENLYPYLGPSTLDRDPQDIIVFVIGGATYEAL	480
Qy	517 TVYNLNRTTPGVRIVLGGTVHNTKSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	481 TVYNLNRTTPGVRIVLGGTVHNTKSFLEEVLASGLHSRSKESQVTSRSASRR	534

RESULT 14

US-11-443-428A-739001

; Sequence 739001, Application US/11443428A

;
 Patent No. 7745391
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hanqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443,428A
 ; CURRENT FILING DATE: 2006-05-31
 ; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 739001
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-443-428A-739001

Query Match	93.9%; Score 2721; DB 3; Length 534;
Best Local Similarity	100.0%;
Matches	534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	37 MVYTQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQEELRRPKTYIYFI 96
Db	1 MVYTQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQEELRRPKTYIYFI 60
Qy	97 YFSNVISKSDVKSLEADEQEVEVVAEYQFQYGYDIAVNPHLFSLNILGCCQGRNWDPQLS 156
Db	61 YFSNVISKSDVKSLEADEQEVEVVAEYQFQYGYDIAVNPHLFSLNILGCCQGRNWDPQLS 120
Qy	157 RTTQGLTALLLSLKCKPMIRYQLSSEAKRLAECVKQVITKEYELFEFRRTEVPPLLL 216
Db	121 RTTQGLTALLLSLKCKPMIRYQLSSEAKRLAECVKQVITKEYELFEFRRTEVPPLLL 180
Qy	217 DRCDDAITPLLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNM 276
Db	181 DRCDDAITPLLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNM 240
Qy	277 YLNFAEIGSNIKNLMEDFQKKKPKEQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVG 336
Db	241 YLNFAEIGSNIKNLMEDFQKKKPKEQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVG 300
Qy	337 ELSRLVSENRNLLEVSEVEQELACQNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYE 396
Db	301 ELSRLVSENRNLLEVSEVEQELACQNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYE 360
Qy	397 RHSSNLSPLGMMDLRNKGVSEKYRKLVSAVVEYGGKVRGRSDLFSPKDAVIAITKQFLKGL 456
Db	361 RHSSNLSPLGMMDLRNKGVSEKYRKLVSAVVEYGGKVRGRSDLFSPKDAVIAITKQFLKGL 420
Qy	457 KGVENVYTQHQPFLHETLDHLIKGRLKENLYPYLGPSTLDRPQDIIVFVIGGATYEAL 516
Db	421 KGVENVYTQHQPFLHETLDHLIKGRLKENLYPYLGPSTLDRPQDIIVFVIGGATYEAL 480
Qy	517 TVYNLNRTTPGVRIVLGGTTVHNTKSFLEEVLASGLHRSRSKESSQVTSRSASRR 570
Db	481 TVYNLNRTTPGVRIVLGGTTVHNTKSFLEEVLASGLHRSRSKESSQVTSRSASRR 534

RESULT 15

US-11-443-428A-739004
; Sequence 739004, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443, 428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 739004
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-739004

Query Match 88.0%; Score 2550; DB 3; Length 526;
Best Local Similarity 100.0%;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61 EIMKHLKAICFLRPTKENVDYI IQELRRPKTYIYIFIYFSNVISKSDVKS LAEADEQE VVA	120
Db	61 EIMKHLKAICFLRPTKENVDYI IQELRRPKTYIYIFIYFSNVISKSDVKS LAEADEQE VVA	120
Qy	121 EVQEFGYGDYIAVNPHLFLSNI LGCCQGRNWDPAQLSRTT QGLTALLLSKKCPMIRYQLS	180
Db	121 EVQEFGYGDYIAVNPHLFLSNI LGCCQGRNWDPAQLSRTT QGLTALLLSKKCPMIRYQLS	180
Qy	181 SEAAKRLAECVKQVITKEYELFEFRRTEVPPPLLILDR CDDA ITPLLNQWTYQAMVHELL	240
Db	181 SEAAKRLAECVKQVITKEYELFEFRRTEVPPPLLILDR CDDA ITPLLNQWTYQAMVHELL	240
Qy	241 GINNNRIDLSRVPGISKDLREVVL SAENDEFYANNM YLNAEIGSNIKNL MEDFQKKPK	300
Db	241 GINNNRIDLSRVPGISKDLREVVL SAENDEFYANNM YLNAEIGSNIKNL MEDFQKKPK	300
Qy	301 EQQKLESIADMKA FVENYPQFKKMSGTVS KHVTVVGELS RL VSERNLLEVSEVEQELACQ	360
Db	301 EQQKLESIADMKA FVENYPQFKKMSGTVS KHVTVVGELS RL VSERNLLEVSEVEQELACQ	360
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSN SLPGLMM DLRNKGVSEKYR	420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSN SLPGLMM DLRNKGVSEKYR	420
Qy	421 KLVS AVVEYGGKRVRGSDLFSPKDAV AITKQFLKGLKG VENVYTQHQPF LHETLDHLIKG	480
Db	421 KLVS AVVEYGGKRVRGSDLFSPKDAV AITKQFLKGLKG VENVYTQHQPF LHETLDHLIKG	480
Qy	481 RLKENLYPYLGPSTLRDRP 499	
Db	481 RLKENLYPYLGPSTLRDRP 499	

Search completed: December 3, 2010, 11:43:49
Job time : 57 secs

..... SCORE 3.0

SCORE Search Results Details for Application 09556178 and Search Result 20101203_114248_us-09-556-178-1.rapbm.

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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:43:00 ; Search time 201 Seconds
(without alignments)
3841.159 Million cell updates/sec

Title: US-09-556-178-1
Perfect score: 2898
Sequence: 1 MNVVFAVKQYISKMIEDSGP.....GLHSRSKESQVTSRSASRR 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6210261 seqs, 1354514112 residues

Total number of hits satisfying chosen parameters: 6210261

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:
1: /ABSS/Data/CRF/ptodata/1/pubpaa/US07_PUBCOMB.pep:*2: /ABSS/Data/CRF/ptodata/1/pubpaa/US08_PUBCOMB.pep:*3: /ABSS/Data/CRF/ptodata/1/pubpaa/US09_PUBCOMB.pep:*4: /ABSS/Data/CRF/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*5: /ABSS/Data/CRF/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*6: /ABSS/Data/CRF/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*7: /ABSS/Data/CRF/ptodata/1/pubpaa/US11B_PUBCOMB.pep:*8: /ABSS/Data/CRF/ptodata/1/pubpaa/US12_PUBCOMB.pep:*SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2898	100.0	570	4 US-10-788-792-187	Sequence 187, Ap
2	2898	100.0	570	5 US-10-511-937-2612	Sequence 2612, Ap
3	2898	100.0	570	5 US-10-219-051B-7142	Sequence 7142, Ap
4	2898	100.0	570	5 US-10-917-503-15151	Sequence 15151, A
5	2898	100.0	570	6 US-11-371-354-75315	Sequence 75315, A
6	2898	100.0	570	6 US-11-443-428A-738990	Sequence 738990,
7	2898	100.0	570	6 US-11-443-428A-738993	Sequence 738993,
8	2898	100.0	570	6 US-11-443-428A-738994	Sequence 738994,
9	2898	100.0	570	6 US-11-443-428A-739003	Sequence 739003,

10	2898	100.0	570	7	US-11-706-155-684	Sequence 684, App
11	2898	100.0	570	8	US-12-584-615-2612	Sequence 2612, Ap
12	2840	98.0	570	5	US-10-219-051B-7140	Sequence 7140, Ap
13	2815.5	97.2	578	5	US-10-450-763-34837	Sequence 34837, A
14	2783	96.0	552	6	US-11-443-428A-738991	Sequence 738991,
15	2777	95.8	552	6	US-11-443-428A-738998	Sequence 738998,
16	2769	95.5	612	6	US-11-443-428A-739002	Sequence 739002,
17	2721	93.9	534	6	US-11-443-428A-738992	Sequence 738992,
18	2721	93.9	534	6	US-11-443-428A-739001	Sequence 739001,
19	2550	88.0	526	6	US-11-443-428A-739004	Sequence 739004,
20	1873	64.6	372	6	US-11-443-428A-738999	Sequence 738999,
21	1755	60.6	359	6	US-11-443-428A-738995	Sequence 738995,
22	1584	54.7	574	6	US-11-097-143-18048	Sequence 18048, A
23	1310	45.2	441	5	US-10-450-763-34838	Sequence 34838, A
24	1299.5	44.8	567	5	US-10-449-902-43905	Sequence 43905, A
25	1286	44.4	568	4	US-10-437-963-112637	Sequence 112637,
26	1286	44.4	568	5	US-10-437-963-112637	Sequence 112637,
27	1273	43.9	567	6	US-11-241-607-62939	Sequence 62939, A
28	1273	43.9	567	8	US-12-435-281-62939	Sequence 62939, A
29	1270	43.8	567	8	US-12-286-964-7714	Sequence 7714, Ap
30	1089	37.6	567	4	US-10-425-115-238853	Sequence 238853,
31	1089	37.6	567	5	US-10-425-115-238853	Sequence 238853,
32	1030.5	35.6	212	4	US-10-425-115-348394	Sequence 348394,
33	1030.5	35.6	212	5	US-10-425-115-348394	Sequence 348394,
34	976	33.7	577	3	US-09-801-368-420	Sequence 420, App
35	976	33.7	577	3	US-09-800-863-420	Sequence 420, App
36	976	33.7	577	5	US-10-309-407-420	Sequence 420, App
37	917	31.6	398	5	US-10-703-032-125739	Sequence 125739,
38	788	27.2	162	6	US-11-443-428A-739006	Sequence 739006,
39	757.5	26.1	200	6	US-11-443-428A-738996	Sequence 738996,
40	753	26.0	364	5	US-10-449-902-35619	Sequence 35619, A
41	744	25.7	158	6	US-11-443-428A-739005	Sequence 739005,
42	671.5	23.2	303	4	US-10-425-115-238857	Sequence 238857,
43	671.5	23.2	303	5	US-10-425-115-238857	Sequence 238857,
44	613	21.2	129	6	US-11-443-428A-739000	Sequence 739000,
45	574	19.8	219	7	US-11-360-355-123305	Sequence 123305,

ALIGNMENTS

RESULT 1

US-10-788-792-187

; Sequence 187, Application US/10788792
; Publication No. US20040191819A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
; FILE REFERENCE: 5152
; CURRENT APPLICATION NUMBER: US/10/788,792
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,655
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 187
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-788-792-187

Query Match 100.0%; Score 2898; DB 4; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
Qy	61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIIFYFNSNVISKSDVKS LAEADEQE VVA 120
Db	61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIIFYFNSNVISKSDVKS LAEADEQE VVA 120
Qy	121 EVQEFGDYIAVNPHLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
Db	121 EVQEFGDYIAVNPHLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
Qy	181 SEA AKRLAECVKQVITKEYELFEFRRTEVPPPLLILDRCD DAITPLLNQWTYQAMVHELL 240
Db	181 SEA AKRLAECVKQVITKEYELFEFRRTEVPPPLLILDRCD DAITPLLNQWTYQAMVHELL 240
Qy	241 GINNNRIDLSRVPGISKD LREV VLA SAE NDEF YAN NM YLN FAE IGS NI KNL MED F QKK PK 300
Db	241 GINNNRIDLSRVPGISKD LREV VLA SAE NDEF YAN NM YLN FAE IGS NI KNL MED F QKK PK 300
Qy	301 EQQKLESIADMKA FVENY PQFKKMS GTVSKHVT VVGELS RL VSER NLLEV SE VE QELAC Q 360
Db	301 EQQKLESIADMKA FVENY PQFKKMS GTVSKHVT VVGELS RL VSER NLLEV SE VE QELAC Q 360
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKGVSEK YR 420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKGVSEK YR 420
Qy	421 KLVS AVE YGGK RVRG SDLFSPKDAV AITKQFLKG LKG VEN VY TQHQ PFL HET LDH LIKG 480
Db	421 KLVS AVE YGGK RVRG SDLFSPKDAV AITKQFLKG LKG VEN VY TQHQ PFL HET LDH LIKG 480
Qy	481 RLKENLYP YLG PSTL RDRP QDIIIVF VIGGAT YEE ALTVY NLN RTTPG VRIV LG GTT VHNT 540
Db	481 RLKENLYP YLG PSTL RDRP QDIIIVF VIGGAT YEE ALTVY NLN RTTPG VRIV LG GTT VHNT 540
Qy	541 KSFLEEV LAS GLHSRS KESS QVT SRSA SRR 570
Db	541 KSFLEEV LAS GLHSRS KESS QVT SRSA SRR 570

RESULT 2

US-10-511-937-2612

; Sequence 2612, Application US/10511937

; Publication No. US20060088836A1

; GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

; FILE REFERENCE: 506612000104

; CURRENT APPLICATION NUMBER: US/10/511,937

; CURRENT FILING DATE: 2004-10-19

; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2003-04-24

; PRIOR APPLICATION NUMBER: US 10/131,831

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: US 10/325,899

; PRIOR FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 3117

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2612
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2612

```

Query Match          100.0%; Score 2898; DB 5; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0

y      1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGISMVYTQSEILQKEVYLFERIDSQRN 60
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
b      1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGISMVYTQSEILQKEVYLFERIDSQRN 60
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
y      61 EIMKHLKAICFLRPTKENVDI IQELRRPKTYIIFYFSNVISKSDVKS LAEADEQEVV 120
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
b      61 EIMKHLKAICFLRPTKENVDI IQELRRPKTYIIFYFSNVISKSDVKS LAEADEQEVV 120
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
y      121 EVQEFGYGDIAVNPHFLS NLGCCGGRNWDPQLSRTTQGLTALLLS LKKCPMIRYQLS 180
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
b      121 EVQEFGYGDIAVNPHFLS NLGCCGGRNWDPQLSRTTQGLTALLLS LKKCPMIRYQLS 180
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
y      181 SEAAKRLAECVKQVITKEYELFEFRRTEVPPPLLILDRCDDAITPLLNQWTYQAMVHELL 240
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
b      181 SEAAKRLAECVKQVITKEYELFEFRRTEVPPPLLILDRCDDAITPLLNQWTYQAMVHELL 240
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
y      241 GINNNRIDLSSRVPGISKDLREVVLSAENDEFYANMYLNFAEIGSNIKNLMEDFQKKPK 300
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
b      241 GINNNRIDLSSRVPGISKDLREVVLSAENDEFYANMYLNFAEIGSNIKNLMEDFQKKPK 300
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
y      301 EQQQKLESIADMKA FVENYQPQFKKMSGTVKHVTVGELSRLVSE RNLLEVSEVEQELACQ 360
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
b      301 EQQQKLESIADMKA FVENYQPQFKKMSGTVKHVTVGELSRLVSE RNLLEVSEVEQELACQ 360
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
y      361 NDHSSALQN KI RLLQNPKVTEFDAARL VMLYALHYERHSSNSLPGLMM DLRNKGVSE YKR 420
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
b      361 NDHSSALQN KI RLLQNPKVTEFDAARL VMLYALHYERHSSNSLPGLMM DLRNKGVSE YKR 420
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
y      421 KLVS AVVEYGGKRVRGSDLFPKDAVITA TQFLKGLKG VENVY TQHQPF LHE TLDH LIKG 480
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
b      421 KLVS AVVEYGGKRVRGSDLFPKDAVITA TQFLKGLKG VENVY TQHQPF LHE TLDH LIKG 480
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
y      481 RLKENLYPILGPSTLDRDPQDIIVFVI GGATYEALTVYLNRLTPGV RIVLG GTTV HNT 540
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
b      481 RLKENLYPILGPSTLDRDPQDIIVFVI GGATYEALTVYLNRLTPGV RIVLG GTTV HNT 540
|||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||||.....|||
y      541 KSFLEEV LASGLHSRSK ESSQVTSRSASRR 570
|||.....|||||.....|||||.....|||
b      541 KSFLEEV LASGLHSRSK ESSQVTSRSASRR 570
|||.....|||||.....|||

```

RESULT 3

US-10-219-051B-7142
; Sequence 7142, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347

;
 PRIORITY FILING DATE: 2001-11-26
 ; NUMBER OF SEQ ID NOS: 14715
 ; SOFTWARE: Perl script
 ; SEQ ID NO 7142
 ; LENGTH: 570
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: Refseq / NP_009189
 ; DATABASE ENTRY DATE: 2002-11-04
 US-10-219-051B-7142

Query Match	100.0%	Score 2898;	DB 5;	Length 570;
Best Local Similarity	100.0%			
Matches	570;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MNNVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQRN	60	
Db	1	QYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQRN	60	
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIYFIYFSNVISKSDVKS LAEADEQE VVA	120	
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIYFIYFSNVISKSDVKS LAEADEQE VVA	120	
Qy	121	EVQEFGYGDYIAVNPHLFSNLILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS	180	
Db	121	EVQEFGYGDYIAVNPHLFSNLILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS	180	
Qy	181	SEAAKRLAECVKQVITKEYELFEPFRTEVPPLLLIDRCDDA ITPLLNQWTYQAMVHELL	240	
Db	181	SEAAKRLAECVKQVITKEYELFEPFRTEVPPLLLIDRCDDA ITPLLNQWTYQAMVHELL	240	
Qy	241	GINNNRIDLSRVPGISKDLEVVLSAEINDEFYANNNMLNFAEIGSNIKNL MEDFQKKPK	300	
Db	241	GINNNRIDLSRVPGISKDLEVVLSAEINDEFYANNNMLNFAEIGSNIKNL MEDFQKKPK	300	
Qy	301	EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLLEVSEVEQELACQ	360	
Db	301	EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLLEVSEVEQELACQ	360	
Qy	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKGVSEK YR	420	
Db	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKGVSEK YR	420	
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKD AVAITKQFLKG LKG VENVYTQHQPF LHETLDH LIKG	480	
Db	421	KLVSAVVEYGGKRVRGSDLFSPKD AVAITKQFLKG LKG VENVYTQHQPF LHETLDH LIKG	480	
Qy	481	RLKENLYPVLGPSTLDRDPQD IIVFVIGGATYE EALT VYNLN R TTPGVRIVLG GTTVHNT	540	
Db	481	RLKENLYPVLGPSTLDRDPQD IIVFVIGGATYE EALT VYNLN R TTPGVRIVLG GTTVHNT	540	
Qy	541	KSFLEEVLASGLHRSRSKES SQVTSRSASRR	570	
Db	541	KSFLEEVLASGLHRSRSKES SQVTSRSASRR	570	

RESULT 4

US-10-917-503-15151
 ; Sequence 15151, Application US/10917503
 ; Publication No. US20070105122A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OTA, TOSHIO
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: NISHIKAWA, TETSUO
 ; APPLICANT: HAYASHI, KOJI
 ; APPLICANT: SAITO, KAORU

; APPLICANT: YAMAMOTO, JUNICHI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: OTSUKI, TETSUJI
 ; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
 ; FILE REFERENCE: 084335/0123
 ; CURRENT APPLICATION NUMBER: US/10/917,503
 ; CURRENT FILING DATE: 2004-08-13
 ; PRIOR APPLICATION NUMBER: US/09/629,469
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: JP 1999-248036
 ; PRIOR FILING DATE: 1999-07-29
 ; PRIOR APPLICATION NUMBER: JP 1999-300253
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: JP 2000-118776
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: JP 2000-183767
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: JP 2000-241899
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/159,590
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: 60/183,322
 ; PRIOR FILING DATE: 2000-02-17
 ; NUMBER OF SEQ ID NOS: 19025
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15151
 ; LENGTH: 570
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-917-503-15151

Query Match 100.0%; Score 2898; DB 5; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
Qy	61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYIFIYSNVISKSVDVKSLSAEADEQEVVVA 120
Db	61 EIMKHLKAICFLRPTKENVDIYIQLERRPKYTIYIFIYSNVISKSVDVKSLSAEADEQEVVVA 120
Qy	121 EVQEFGYDGYIAVNPHFLSNIILGCCQGRNWDPQLSRTTQGLTALLSSLKKCPMIRYQLS 180
Db	121 EVQEFGYDGYIAVNPHFLSNIILGCCQGRNWDPQLSRTTQGLTALLSSLKKCPMIRYQLS 180
Qy	181 SEAARKLAECKVKQVITKEYELFEFRRTEVPPLLILDRCCDAITPPLNQWTYQAMVHELL 240
Db	181 SEAARKLAECKVKQVITKEYELFEFRRTEVPPLLILDRCCDAITPPLNQWTYQAMVHELL 240
Qy	241 GINNNRIDSLRVPGISKDLREVVLSAENDEFYANNMYLNAEIGSNIKNLMEDFQKKPK 300
Db	241 GINNNRIDSLRVPGISKDLREVVLSAENDEFYANNMYLNAEIGSNIKNLMEDFQKKPK 300
Qy	301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
Db	301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEKYL 420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEKYL 420
Qy	421 KLVSAVVEYGGKVRGSDLFSPKDAVITKQFLKGLKGVENVYTQHQPLHETLDHLIKG 480

Db	421	KLVSAAVEYGGKVRGSDLFSPKDAVITKQFLKGKGVENVYTQHQPFHLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRLDRPQDIIIVFVIIGGATYYEALTVYLNRLTPGVRIVLGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRLDRPQDIIIVFVIIGGATYYEALTVYLNRLTPGVRIVLGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSAASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSAASRR	570

RESULT 5

US-11-371-354-75315

; Sequence 75315, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75315
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-75315

Query Match 100.0%; Score 2898; DB 6; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVYDIIQELRPRKYTIYFIYFSNVISKSDVKS LAEADEQE VVA	120
Db	61	EIMKHLKAICFLRPTKENVYDIIQELRPRKYTIYFIYFSNVISKSDVKS LAEADEQE VVA	120
Qy	121	EVQEFGYGDIAVNPHFLSNIILGCCQGRNWDPQLSRTTQGLTALLLSLKCPMIRYQLS	180
Db	121	EVQEFGYGDIAVNPHFLSNIILGCCQGRNWDPQLSRTTQGLTALLLSLKCPMIRYQLS	180
Qy	181	SEAARKLAECAVKQVITKEYELFEFRRTVEPPPLLILDRCCDAITPLNQWTYQAMVHELL	240
Db	181	SEAARKLAECAVKQVITKEYELFEFRRTVEPPPLLILDRCCDAITPLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVL SAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300

Db	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 300
Qy	301 EQQKLESIADMKAFFVENYQPQFKKMSGTVKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
Db	301 EQQKLESIADMKAFFVENYQPQFKKMSGTVKHVTVVGELSRLVSERNLLLEVSEVEQELACQ 360
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEKYL 420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEKYL 420
Qy	421 KLVSAVVEYGGKVRGSDLFSPKDAAVITKQFLKGLKGKVENVYTQHQPLHETLDHLIKG 480
Db	421 KLVSAVVEYGGKVRGSDLFSPKDAAVITKQFLKGLKGKVENVYTQHQPLHETLDHLIKG 480
Qy	481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYYEALT VYLNRLTPGV RIVLGGTTVHN T 540
Db	481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYYEALT VYLNRLTPGV RIVLGGTTVHN T 540
Qy	541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
Db	541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

RESULT 6

US-11-443-428A-738990

; Sequence 738990, Application US/11443428A
; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hanqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738990

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738990

Query Match 100.0%; Score 2898; DB 6; Length 570;
 Best local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQRN 60

Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQRN 60

Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRPRKYTIYFIYFSNVISKSDVKS LAEADEQE VVA 120

Db 61 EIMKHLKAICFLRPTKENVDYIIQELRPRKYTIYFIYFSNVISKSDVKS LAEADEQE VVA 120

Qy 121 EVQEFGYGDYIAVNPHLFLS NILGCCQGRNWDP AQLSRTT QGLT ALLSLK KCPMIR YQLS 180

Db 121 EVQEFGYGDYIAVNPHLFLS NILGCCQGRNWDP AQLSRTT QGLT ALLSLK KCPMIR YQLS 180

Qy	181	SEAAKRLAECVKQVITKEYELFERRTEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFERRTEVPPLLLILDRCCDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Qy	361	NNDHSSALQNIRKLQLNPQPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEKYR	420
Db	361	NNDHSSALQNIRKLQLNPQPKVTEFDAARLVMLYALHYERHSSNLPGLMMMDLRNKGVSEKYR	420
Qy	421	KLVSAVVEYGGKVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFHLHETLDHLIKG	480
Db	421	KLVSAVVEYGGKVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFHLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEALTVYLNRLTPGVRLVGGTTVHN	540
Db	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEALTVYLNRLTPGVRLVGGTTVHN	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570

RESULT 7

US-11-443-428A-738993

; Sequence 738993, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738993

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738993

Query Match 100.0%; Score 2898; DB 6; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFVAKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60

Db	1	MNVVFVAKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
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Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIYFIYFSNVISKSDVKS LAEADEQE VVA	120
----	----	--	-----

Db	61 EIMKHLKAICFLRPTKENVDYI IQELRPRKYTIYFIYFSNVISKSDVKS LAEADEQEVVA	120
Qy	121 EVOEFYGDYIAVNPHLSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121 EVQEFYGDYIAVNPHLSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181 SEAARKLAEACVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLNQWTYQAMVHELL	240
Db	181 SEAARKLAEACVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLNQWTYQAMVHELL	240
Qy	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Db	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Qy	301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLLEVSEVEQELACQ	360
Db	301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLLEVSEVEQELACQ	360
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSN SLPGLMMMDLRNKGVSEK YR	420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSN SLPGLMMMDLRNKGVSEK YR	420
Qy	421 KLVSAVVEYGGKRVRGSDLFSPKD AVAITKQFLKGLKG VENVYTQHQPF LHETLDHLIK G	480
Db	421 KLVSAVVEYGGKRVRGSDLFSPKD AVAITKQFLKGLKG VENVYTQHQPF LHETLDHLIK G	480
Qy	481 RLKENLYPILGPSTLDRPQDIIIVFVI GGATYE EALT VYVNLNR TPPGV RIVLGTTVHN T	540
Db	481 RLKENLYPILGPSTLDRPQDIIIVFVI GGATYE EALT VYVNLNR TPPGV RIVLGTTVHN T	540
Qy	541 KSFLEEVLASGLHSRSKES SQVTSRSASRR	570
Db	541 KSFLEEVLASGLHSRSKES SQVTSRSASRR	570

RESULT 8

US-11-443-428A-738994

; Sequence 738994, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hanqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443,428A
 ; CURRENT FILING DATE: 2006-05-31
 ; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 738994
 ; LENGTH: 570
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-11-443-428A-738994

Query Match 100.0%; Score 2898; DB 6; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQNR 60
Db	1
Qy	61 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQNR 60
Db	61
Qy	61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIIFYFSNVISKSDVKS LAEADEQE VVA 120
Db	61
Qy	121 EVQEFGDYIAVNPHLFSLNILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180
Db	121
Qy	181 SEAARKLAEVCVKQVITKEYELFEFRTEVPPPLLILLDRCDDAITPLLNQWTYQAMVHELL 240
Db	181
Qy	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNL MEDFQKKPK 300
Db	241
Qy	301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVTVVGELSRLVSE RNLLLEVSEVEQELACQ 360
Db	301
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSN SLPGLMMMDLRNKGVSEK YR 420
Db	361
Qy	421 KLVS AVVEYGGKRVRGSDLFSPKD AVAITKQFLKGLKG VENVTQHQPF LHETLDH LIKG 480
Db	421
Qy	481 RLKENLYYLGPSTL RDRPQDIIIVEVIGGATYEALTVY NLNRTTPGV RIVLGGTTVHN T 540
Db	481
Qy	541 KSFLEEVLASGLHSRSKES SQVTSRSASRR 570
Db	541

RESULT 9

US-11-443-428A-739003

; Sequence 739003, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 739003

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens
US-11-443-428A-739003

Query Match 100.0%; Score 2898; DB 6; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
|||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIYFIYFSNVISKSDVKS LAEADQE VVA 120
|||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKTYIYFIYFSNVISKSDVKS LAEADQE VVA 120
|||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 EVQE FYG DYIAVNPHLFSLN ILGCCQGR NWDP AQLS RTT QGL TALLLSLKCP MIR YQLS 180
|||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 EVQE FYG DYIAVNPHLFSLN ILGCCQGR NWDP AQLS RTT QGL TALLLSLKCP MIR YQLS 180
|||||||||||||||||||||||||||||||||||||||||||
Qy 181 SEA AKRLAECV KVQ VITKEYEL FFR TVE PPLL LLDRC DDA ITPL LNQ WTYQ AMV HELL 240
|||||||||||||||||||||||||||||||||||||||||||||||
Db 181 SEA AKRLAECV KVQ VITKEYEL FFR TVE PPLL LLDRC DDA ITPL LNQ WTYQ AMV HELL 240
|||||||||||||||||||||||||||||||||||||||
Qy 241 GINNNRIDLSR VPG I SKDL R E VVLSA E NDEF YAN NM YLNF AEIG SNI KNL MEDF QKK PK 300
|||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GINNNRIDLSR VPG I SKDL R E VVLSA E NDEF YAN NM YLNF AEIG SNI KNL MEDF QKK PK 300
|||||||||||||||||||||||||||||||||||
Qy 301 EQ QK L EISIADM KAFV ENY P QFK KM SGTV SKH VT VVG ELS RL VSER NL LEV SE VE QEL ACQ 360
|||||||||||||||||||||||||||||||||||||||||||
Db 301 EQ QK L EISIADM KAFV ENY P QFK KM SGTV SKH VT VVG ELS RL VSER NL LEV SE VE QEL ACQ 360
|||||||||||||||||||||||||||||||
Qy 361 NDHSSALQNIKR LLQNPKVTEFDAARLVM LYALHYERHSSNSLPGLMM DLRNKG VSE KYR 420
|||||||||||||||||||||||||||||||||||||||
Db 361 NDHSSALQNIKR LLQNPKVTEFDAARLVM LYALHYERHSSNSLPGLMM DLRNKG VSE KYR 420
|||||||||||||||||||||||||||
Qy 421 KLV SAVVEYGGK RVG SDSL FSPK DAVA ITKQFLK GLKG VEN VYTQHQ PFLHET LDH LIKG 480
|||||||||||||||||||||||||||||||||||||||
Db 421 KLV SAVVEYGGK RVG SDSL FSPK DAVA ITKQFLK GLKG VEN VYTQHQ PFLHET LDH LIKG 480
|||||||||||||||||||||||
Qy 481 RLK ENLYP YLG PSTL RDR PQD II VEV FVIGGAT YEE ALTV YNL NR RT PG VRIV LG GT TV HNT 540
|||||||||||||||||||||||||||||||||||
Db 481 RLK ENLYP YLG PSTL RDR PQD II VEV FVIGGAT YEE ALTV YNL NR RT PG VRIV LG GT TV HNT 540
|||||||||||||||||||||||
Qy 541 KSFLEEV LASGLHSRSK ESSQV TSRSASRR 570
|||||||||||||||||||
Db 541 KSFLEEV LASGLHSRSK ESSQV TSRSASRR 570

RESULT 10

US-11-706-155-684

; Sequence 684, Application US/11706155

; Publication No. US20080075722A1

; GENERAL INFORMATION

; APPLICANT: DEPINHO, RONALD A.

; APPLICANT: ANDERSON, KENNETH C.

; APPLICANT: CARRASCO, DANIEL R.

; APPLICANT: TONON, GIOVANNI

; APPLICANT: BRENNAN, CAMERON

; APPLICANT: SHAUGHNESSY, JOHN D., Jr.

; APPLICANT: CHIN, LYNDIA

; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,

; TITLE OF INVENTION: PREVENTION, AND THERAPY OF CANCER

; FILE REFERENCE: DFS-065.01

; CURRENT APPLICATION NUMBER: US/11/706,155

; CURRENT FILING DATE: 2007-11-09

; PRIOR APPLICATION NUMBER: 60/773,072

; PRIOR FILING DATE: 2006-02-14

; NUMBER OF SEQ ID NOS: 713
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 684
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-706-155-684

Query Match 100.0%; Score 2898; DB 7; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQNR 60
Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQNR 60

Qy 61 EIMKHLKAICFLRPTKENVDDIIQELRPRKYTIYIYFSNVISKSDVKS LAEADEQEVV A 120
Db 61 EIMKHLKAICFLRPTKENVDDIIQELRPRKYTIYIYFSNVISKSDVKS LAEADEQEVV A 120

Qy 121 EVQEFYGDYIAVNPHLFLSNI LGCCQGRNWDPQLSRTTQGLTALLLSLKCPMIRYQLS 180
Db 121 EVQEFYGDYIAVNPHLFLSNI LGCCQGRNWDPQLSRTTQGLTALLLSLKCPMIRYQLS 180

Qy 181 SEAARKLAECVKQVITKEYELFEFRRTEVPPLLILDRCDDAITPLLNQWTYQAMVHELL 240
Db 181 SEAARKLAECVKQVITKEYELFEFRRTEVPPLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy 241 GINNNRIDLSRVPGISKDREV VLSAENDEFYANNMYLNF AEIGSNIKNL MEDFQKKPK 300
Db 241 GINNNRIDLSRVPGISKDREV VLSAENDEFYANNMYLNF AEIGSNIKNL MEDFQKKPK 300

Qy 301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVT VVGEL SRLVSE RNLLLEV SEVE QELACQ 360
Db 301 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVT VVGEL SRLVSE RNLLLEV SEVE QELACQ 360

Qy 361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKG VSEK YR 420
Db 361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMM DLRNKG VSEK YR 420

Qy 421 KLVSAAVVEYGGKRVRGSDLFSPKDAV AITKQFLKG LKG VENVYTQHQPF LHETLDH LING 480
Db 421 KLVSAAVVEYGGKRVRGSDLFSPKDAV AITKQFLKG LKG VENVYTQHQPF LHETLDH LING 480

Qy 481 RLKENLYPYLGPSTL RDRPQD IIVFVI GGATYEAEALT VYNL NR RTPG VRIVLG GTTVHNT 540
Db 481 RLKENLYPYLGPSTL RDRPQD IIVFVI GGATYEAEALT VYNL NR RTPG VRIVLG GTTVHNT 540

Qy 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
Db 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

RESULT 11

US-12-584-615-2612

; Sequence 2612, Application US/12584615

; Publication No. US20100151467A1

; GENERAL INFORMATION

; APPLICANT: Xdx, INC.

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

;
 TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
 ; FILE REFERENCE: 506612000123
 ; CURRENT APPLICATION NUMBER: US/12/584,615
 ; CURRENT FILING DATE: 2009-09-23
 ; PRIOR APPLICATION NUMBER: US 10/511,937
 ; PRIOR FILING DATE: 2005-07-22
 ; PRIOR APPLICATION NUMBER: PCT/US2003/12946
 ; PRIOR FILING DATE: 2003-04-24
 ; PRIOR APPLICATION NUMBER: US 10/325,899
 ; PRIOR FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 10/131,831
 ; PRIOR FILING DATE: 2002-04-24
 ; NUMBER OF SEQ ID NOS: 13083
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2612
 ; LENGTH: 570
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-12-584-615-2612

Query Match 100.0%; Score 2898; DB 8; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
Qy	61 EIMKHLKAICFLRPTKENVDYIIQELRPRKYTIYIYFSNVISKSDVKSLSAEADEQEVVVA 120
Db	61 EIMKHLKAICFLRPTKENVDYIIQELRPRKYTIYIYFSNVISKSDVKSLSAEADEQEVVVA 120
Qy	121 EVQEFGYGDYIAVNPHLFLSNIILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180
Db	121 EVQEFGYGDYIAVNPHLFLSNIILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180
Qy	181 SEAARKLAECVKQVITKEYLEFRRTEVPPPLLILDRCDDAITPLLNQWTYQAMVHELL 240
Db	181 SEAARKLAECVKQVITKEYLEFRRTEVPPPLLILDRCDDAITPLLNQWTYQAMVHELL 240
Qy	241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 300
Db	241 GINNNRIDLSRVPGISKDLREVVLSEARNLLEVSEVEQELACQ 300
Qy	301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
Db	301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
Qy	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERISSNSLPGLMMMDLRNKGVSEKYL 420
Db	361 NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERISSNSLPGLMMMDLRNKGVSEKYL 420
Qy	421 KLVSAAVVEYGGKRVRGSDLFSPKDAAVITKQFLKGLKGVENYTTQHQPLHETLDHLIKG 480
Db	421 KLVSAAVVEYGGKRVRGSDLFSPKDAAVITKQFLKGLKGVENYTTQHQPLHETLDHLIKG 480
Qy	481 RLKENLYPILGPSTLDRDPQDIIVFVIAGGATYYEALTVYVNLNRTPGVIRVLGGTTVHN 540
Db	481 RLKENLYPILGPSTLDRDPQDIIVFVIAGGATYYEALTVYVNLNRTPGVIRVLGGTTVHN 540
Qy	541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
Db	541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

RESULT 12

US-10-219-051B-7140

; Sequence 7140, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: Lea 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 7140
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAB53041
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-7140

Query Match 98.0%; Score 2840; DB 5; Length 570;
Best Local Similarity 97.2%;
Matches 554; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

Qy	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQNR 60
	: : : : : : : : : : :
Db	1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQNR 60
Qy	61 EIMKHLKAICFLRPTKENVDYIIQELRPRKYTIYIFIYFSNVISKSDVKS LAEADEQE VVA 120
	: : : : : : : : : : : :
Db	61 EIMKHLKAICFLRPTKENVDSL I QELRPRKYSIYIFIYFSNVISKSDVKS LAEADEQE VVA 120
Qy	121 EVQEFGYGDYIAVNPHLFSLNILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180
	: : : : : : : : : : :
Db	121 EVQEFGYGDYIAVNPHLFSLNILGCCQGRNWDPQLSRTTQGLTALLSLKKCPMIRYQLS 180
Qy	181 SEAARKLAEACVVKQVITKEYELFEFRRTEVPPPLLILDRCDDAITPLLNQWTYQAMVHELL 240
	: : : : : : : : : : : :
Db	181 SEAARKLGE CVVKQVISKEYELFEFRRTEVPPPLLILDRCDDAITPLLNQWTYQAMVHELL 240
Qy	241 GINNNRIDLSRVPGISKDLREV VLSAENDEFYANMMYLNFAEIGSNIKNL MEDFQKKPK 300
	: : : : : : : : : : :
Db	241 GINNNRIDLSRVPGISKDLREV VLSAENDEFYANMMYLNFAEIGSNIKNL MEDFQKKRPK 300
Qy	301 EQQKLESIADMKA FVENYQPQFKMSGTVSKHVT VVGELSRLVSE RNLLLEVSE VEQELACQ 360
	: : : : : : : : : : :
Db	301 EQQKLESIADMKA FVENYQPQFKMSGTVSKHVT VVGELSRLVSE RNLLLEVSE VEQELACQ 360
Qy	361 NDHSSALQNICKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLMMDL RNKGVSEK YR 420
	: : : : : : : : : : : :
Db	361 NDHSSALQNICKRLLQNPKVTEFDAARLVMLYALHYERHSSNLPGLIVD LRSKGVAEK YR 420
Qy	421 KLVSAVVEYGGKVRGSDLFSPKD AVAITKQF LKLKG VENVYTQHQPLHETLDH LIKG 480
	: : : : : : : : : : :
Db	421 KLVSAVVEYGGKVRGSDLFSPKD AVAITKQF LKLKG VENVYTQHQPLHETLDH LIKG 480
Qy	481 RLKENLYPFLGPSTL RDRPQDI IFVPIGGATYEEA LT VYNLNRTTPGVRIVLG GTT VHNT 540
	: : : : : : : : : : : :
Db	481 RLKENLYPFLGPSTL RDRPQDI IFVPIGGATYEEA LT VYNLNRTTPGVRIVLG GTT VHNT 540
Qy	541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

Db 541 KSFLEEVLASGLHSRSRESSQATSRSA SRR 570

RESULT 13
 US-10-450-763-34837
 ; Sequence 34837, Application US/10450763
 ; Publication No. US20050196754A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 ; FILE REFERENCE: 790CIP3/US
 ; CURRENT APPLICATION NUMBER: US/10/450,763
 ; CURRENT FILING DATE: 2003-06-11
 ; PRIOR APPLICATION NUMBER: PCT/US01/08631
 ; PRIOR FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: 09/540,217
 ; PRIOR FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: 09/649,167
 ; PRIOR FILING DATE: 2000-08-23
 ; NUMBER OF SEQ ID NOS: 60736
 ; SOFTWARE: Custom
 ; SEQ ID NO 34837
 ; LENGTH: 578
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (218)..(258)
 ; OTHER INFORMATION: Sec1 family domain identified by eMATRIX, accession number
 ; OTHER INFORMATION: PF00995B, p-value=6.745e-25, raw score of 17.37
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (95)..(562)
 ; OTHER INFORMATION: Sec1 family domain identified by PFam, accession name Sec1, E
 ; OTHER INFORMATION: -value=2.9e-164, PFam score of 559.1
 US-10-450-763-34837

Query Match 97.2%; Score 2815.5; DB 5; Length 578;
 Best Local Similarity 97.7%;
 Matches 558; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 60
 |||||||

Db 8 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVTQSEILQKEVYLFERIDSQRN 67
 |||||||

Qy 61 EIMKHLKAICFLRPTKENVDTIQQELRPRKYTIYIFIYFSNVNISKSDVKS LA-EADEQEVV 119
 ||||||| : : |||||

Db 68 EIMKHLKAICFLRPTKENVDTIQQELRPRKYTIYIFIYFSNVNISKSDV EFIGLKLIEQEVV 127
 |||||||

Qy 120 AEVQE FYG DYIAVNPHFLS NLIGCC QGR NW DPA QLS RTT QGL T ALL LSK KCP MIR YQL 179
 |||||||

Db 128 AEVQE FYG DYIAVNPHFLS NLIGCC QGR NW DPA QLS RTT QGL T ALL LSK KCP MIR YQL 187
 |||||||

Qy 180 SSEAAKRLAECVKQVITKEYELFEFRRTEVPPLL LLDRC DDA ITPLLNQWTYQAMVHEL 239
 |||||||

Db 188 SSEAAKRLAECVKQVITKEYELFEFRRTEVPPLL LLDRLDDA ITPLLNQWTYQAMVHEL 247
 |||||||

Qy 240 LGINNNRIDL SRVPGIS KDLR E VVLS A EDEF YANNM YLN FAE IGSNI KNL MEDF QKK KP 299
 |||||||

Db 248 LGINNNRIDL SRVPGIS KDLR E VVLS A EDEF YANNM YLN FAE IGSNI KNL MEDF QKK KP 307
 |||||||

Qy 300 KEQQKLES IADMKA FVN ENPQF KKMS GTVS KVHTVV GEL SRL VSE RNLL EVSE VE QEL AC 359
 |||||||

Db 308 KEQQKLES IGSMSKA FVN ENPQF KKMS GTVS KVHTVV GEL SRL VSE RNLL EVSE VE QEL AC 367
 |||||||

Qy 360 QNDHSSALQN KRL LQNP KVTE FDA RLVML YALHYERHSSN SLP GLMM DLRN KG VSE KY 419
 |||||||

Db	368	QNDHSSALQNQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKY	427
Qy	420	RKLVSAVVEYGGKVRGSDLFSPKDVAITKQFLKGLKGVENVYTQHQPFHLHETLDHLIK	479
Db	428	RKLVSAVVEYGGKVRGSDLFSPKDVAITKQFLKGLKGVGVNVTQLQPFLHETLDHLIK	487
Qy	480	GRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVDNLNRTTPGVRIVLGGTTVHN	539
Db	488	GRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVDNLNRTTPGVRIVLGGTTVHN	547
Qy	540	TKSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	548	TKSFLEEVLASGLHSRSKESSQVTSRSASRR	578

RESULT 14

US-11-443-428A-738991

; Sequence 738991, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443, 428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738991

; LENGTH: 552

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738991

Query Match 96.0%; Score 2783; DB 6; Length 552;
 Best Local Similarity 96.8%;
 Matches 552; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

Qy 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQRN 60

Db 1 MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQ-- 58

Qy 61 EIMKHLKAICFLRPTKENVYDIIQELRPRKYTIYFIYFSNVISKSVDVKS LAEADEQEVV A 120

Db 59 -----ENVDIYDIIQELRPRKYTIYFIYFSNVISKSVDVKS LAEADEQEVV A 102

Qy 121 EVQEFGYDGYIAVNPHFLS L NILGCCQGRNWDP A QLS RTT QGL T ALL S L K KCPMIRYQLS 180

Db 103 EVQEFGYDGYIAVNPHFLS L NILGCCQGRNWDP A QLS RTT QGL T ALL S L K KCPMIRYQLS 162

Qy 181 SEA AKRLAECVKQVITKEYELFE FRR TEV PPL L L I L D R C D D A I T P L L N Q W T Y Q A M V H E L L 240

Db 163 SEA AKRLAECVKQVITKEYELFE FRR TEV PPL L L I L D R C D D A I T P L L N Q W T Y Q A M V H E L L 222

Qy 241 GINNNRIDLSRVPGISKDLREVVL SA E N D E F Y A N N M Y L N F A E I G S N I K N L M E D F Q K K P K 300

Db 223 GINNNRIDLSRVPGISKDLREVVL SA E N D E F Y A N N M Y L N F A E I G S N I K N L M E D F Q K K P K 282

Qy	301 EQQKLESIADMKA FVENYPQFKMSGT VKHVTVVGELSR LVSERNLLEVSE VQELACQ 360
Db	 283 EQQKLESIADMKA FVENYPQFKMSGT VKHVTVVGELSR LVSERNLLEVSE VQELACQ 342
Qy	361 NDHSSALQNIK RLLQNPKVTEFDA RLVMLYALHYER HSSNLPGLMM DLRNKGVSEKYR 420
Db	 343 NDHSSALQNIK RLLQNPKVTEFDA RLVMLYALHYER HSSNLPGLMM DLRNKGVSEKYR 402
Qy	421 KLVSAVVEYGG KVRGSDLFSPK DAVITA TKQFLKGLGV ENVYTQHQPF LHETLDHLIKG 480
Db	 403 KLVSAVVEYGG KVRGSDLFSPK DAVITA TKQFLKGLGV ENVYTQHQPF LHETLDHLIKG 462
Qy	481 RLKENLYP LGPS TLRDRP QDII IVFVI GGAT YEE ALT V Y LN N RT TP G V R I V L G G T V H N T 540
Db	 463 RLKENLYP LGPS TLRDRP QDII IVFVI GGAT YEE ALT V Y LN N RT TP G V R I V L G G T V H N T 522
Qy	541 KSFLEEV LASGLHSRS KESSQ VTSRS ASRR 570
Db	 523 KSFLEEV LASGLHSRS KESSQ VTSRS ASRR 552

RESULT 15

US-11-443-428A-738998
; Sequence 738998, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738998
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738998

Query Match 95.8%; Score 2777; DB 6; Length 552;
Best Local Similarity 99.3%;
Matches 547; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy	1 MNVVFAVKQYISK MIEDSGPGMKV LLMDKETTGIV SMVYTQSEILQ KEVYLFERIDS SQNR 60
Db	 1 MNVVFAVKQYISK MIEDSGPGMKV LLMDKETTGIV SMVYTQSEILQ KEVYLFERIDS SQNR 60
Qy	61 EIMKHLKAICFL RPTKENV DYIIQELR PKTYI FYSNV ISKSDV KSLAEAD QE VVA 120
Db	 61 EIMKHLKAICFL RPTKENV DYIIQELR PKTYI FYSNV ISKSDV KSLAEAD QE VVA 120
Qy	121 EVQEFGYD YIAVNPH FLSNI LGC GCC QGR NWD PDA QLS RTT QGL TALL LSLK KCP MIRY QLS 180
Db	 121 EVQEFGYD YIAVNPH FLSNI LGC GCC QGR NWD PDA QLS RTT QGL TALL LSLK KCP MIRY QLS 180
Qy	181 SEA AKRLAEC CVKQV ITKEY EFL FRR TEV PPLL LIDRC DDA ITP LNN QWT YQAM VHELL 240

Db	181	SEAAKRLAECKVQVITKEYELFEFRTEVPPLLILDRCDDAITPLLNQWYQAMVHELL	240
Qy	241	GINNNRIDLSRVPKGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Db	241	GINNNRIDLSRVPKGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVGELSRLVSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVGELSRLVSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYL	420
Db	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYL	420
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFHLHETLDHLIKG	480
Db	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFHLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVDYLNRTTPGVRIVLGTTVHNNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVDYLNRTTPGVRIVLGTTVHNNT	540
Qy	541	KS--FLEEVL A 549	
Db	541	KSFRFLREGLA 551	

Search completed: December 3, 2010, 11:46:57
 Job time : 237 secs

SCORE 3.0

SCORE Search Results Details for Application 09556178 and Search Result 20101203_114249_us-09-556-178-1.rapbn.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101203_114249_us-09-556-178-1.rapbn.

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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:55 ; Search time 5 Seconds
(without alignments)
160.331 Million cell updates/sec

Title: US-09-556-178-1

Perfect score: 2898

Sequence: 1 MNVVFAVKQYISKMIEDSGP.....GLHSRSKESSQVTSRSASRR 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 14841 seqs, 1406414 residues

Total number of hits satisfying chosen parameters: 14841

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:
1: /ABSS/Data/CRF/ptodata/1/pubpaa/US10_NEW_PUB.pep:
2: /ABSS/Data/CRF/ptodata/1/pubpaa/US11_NEW_PUB.pep:
3: /ABSS/Data/CRF/ptodata/1/pubpaa/US12_NEW_PUB.pep:
SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	123.5	4.3	980 3	US-12-293-792A-10 Sequence 10, Appli
2	117	4.0	500 3	US-12-441-092-4 Sequence 4, Appli
3	117	4.0	667 3	US-12-441-092-2 Sequence 2, Appli
4	114	3.9	1977 3	US-12-739-689-45 Sequence 45, Appli
5	114	3.9	1977 3	US-12-739-723-39 Sequence 39, Appli
6	113	3.9	1396 3	US-12-086-571-50 Sequence 50, Appli
7	109	3.8	488 3	US-12-086-571-175 Sequence 175, App
8	107.5	3.7	813 3	US-12-739-689-36 Sequence 36, Appli
9	107.5	3.7	2325 3	US-12-739-689-28 Sequence 28, Appli
10	107.5	3.7	2325 3	US-12-739-723-30 Sequence 30, Appli
11	99.5	3.4	2757 3	US-12-625-053A-38 Sequence 38, Appli
12	99	3.4	755 3	US-12-345-877-181 Sequence 181, App
13	97.5	3.4	1960 3	US-12-864-218-90 Sequence 90, Appli
14	96.5	3.3	483 3	US-12-441-092-41 Sequence 41, Appli

15	96.5	3.3	1979	3	US-12-739-689-47	Sequence 47, Appli
16	96.5	3.3	1979	3	US-12-739-723-41	Sequence 41, Appli
17	96	3.3	3692	3	US-12-625-053A-48	Sequence 48, Appli
18	95.5	3.3	1014	3	US-12-345-877-251	Sequence 251, App
19	95	3.3	334	3	US-12-441-092-8	Sequence 8, Appli
20	95	3.3	501	3	US-12-441-092-6	Sequence 6, Appli
21	94	3.2	787	3	US-12-739-689-54	Sequence 54, Appli
22	94	3.2	808	3	US-12-523-023-3	Sequence 3, Appli
23	93.5	3.2	534	3	US-12-764-333A-3	Sequence 3, Appli
24	93.5	3.2	794	3	US-12-523-023-4	Sequence 4, Appli
25	92	3.2	878	3	US-12-733-159A-166	Sequence 166, App
26	91.5	3.2	788	3	US-12-739-689-55	Sequence 55, Appli
27	90.5	3.1	408	3	US-12-441-092-43	Sequence 43, Appli
28	90.5	3.1	872	3	US-12-523-023-1	Sequence 1, Appli
29	88	3.0	303	3	US-12-441-092-40	Sequence 40, Appli
30	88	3.0	332	3	US-12-441-092-39	Sequence 39, Appli
31	88	3.0	2005	3	US-12-317-496-34	Sequence 34, Appli
32	87.5	3.0	913	3	US-12-086-571-250	Sequence 250, App
33	87.5	3.0	1757	3	US-12-787-298-15	Sequence 15, Appli
34	87	3.0	295	3	US-12-625-053A-50	Sequence 50, Appli
35	87	3.0	562	3	US-12-086-571-242	Sequence 242, App
36	87	3.0	2005	3	US-12-317-496-35	Sequence 35, Appli
37	87	3.0	2339	3	US-12-739-689-26	Sequence 26, Appli
38	87	3.0	2339	3	US-12-739-723-26	Sequence 26, Appli
39	87	3.0	2589	3	US-12-739-689-42	Sequence 42, Appli
40	87	3.0	2589	3	US-12-739-723-28	Sequence 28, Appli
41	85.5	3.0	801	3	US-12-784-310-2	Sequence 2, Appli
42	85	2.9	858	3	US-12-682-544-14	Sequence 14, Appli
43	85	2.9	858	3	US-12-625-544-15	Sequence 15, Appli
44	85	2.9	858	3	US-12-682-544-16	Sequence 16, Appli
45	84.5	2.9	530	3	US-12-784-310-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
 US-12-293-792A-10
 ; Sequence 10, Application US/12293792A
 ; Publication No. US20100297178A1
 ; GENERAL INFORMATION
 ; APPLICANT: Murdoch University
 ; TITLE OF INVENTION: Novel Genes and Proteins of Brachyspira hyodysenteriae and Use of
 ; TITLE OF INVENTION:Same for Diagnosis and Therapy
 ; FILE REFERENCE: P78788.US
 ; CURRENT APPLICATION NUMBER: US/12/293,792A
 ; CURRENT FILING DATE: 2010-07-15
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: PatentIn version 3.5
 ; SEQ ID NO 10
 ; LENGTH: 980
 ; TYPE: PRT
 ; ORGANISM: Brachyspira hyodysenteriae
 US-12-293-792A-10

Query Match 4.3%; Score 123.5; DB 3; Length 980;
 Best Local Similarity 18.2%;
 Matches 124; Conservative 106; Mismatches 262; Indels 191; Gaps 26;

Qy 5 FAVKQYISKMIED-----SGPGMKVLLMDKETTGIVSMVTQSEI----- 44
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Db 228 FAIVDEVDSILYLDEARTPLIISGPAEKNIKMYYEIDRIIPML-KQAEVDERMREVAGTGD 286

Qy 45 -----LQKEVYLFER-----IDSQNREIMKHL-KAICFLRPTKENVDYIIQ 84
 | ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 287 YVLDEKDKNVYLTEEGVHKVEKLLNVENLYGAQSSTIVHHVNQALKAHKVFKKDVDYMT 346